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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8652	18541	28825	3.94	3.3E-01	P47953	SWISSPROT	GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (CBP30)
8956	18763		4.79	3.3E-01	AA806621.1	EST_HUMAN	ob71g02s1.NC1_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1336850 3'
8972	10000	19791	1.88	3.3E-01	X07990.1	NT	Rhizobium leguminosarum sym plasmid pRL5J1 nadX gene
9119	18881	28789	1.63	3.3E-01	6598319	NT	Homo sapiens aldehyde oxidase 1 (AOX1), mRNA
9817	19323		6.05	3.3E-01	AP000002.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 287001-544000 nt, position (27)
449	10393		1.98	3.2E-01	AF018281.1	NT	Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds
701	10634		2.05	3.2E-01	AL161561.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 61
1146	11059	20902	18.99	3.2E-01	AF047013.1	NT	Fusarium roseum virus 1 RNA2 putative RNA dependent RNA polymerase gene, complete cds
1261	11168	21019	1.04	3.2E-01	Z502022.1	NT	<i>P. vulgaris</i> arc5-1 gene
1363	11274	21130	6.25	3.2E-01	Q48624	SWISSPROT	LACTOSE PERMEASE (LACTOSE-PROTON SYMPORT) (LACTOSE TRANSPORT PROTEIN)
1737	11638	21506	1.22	3.2E-01	Z38041.1	NT	<i>S.cerevisiae</i> chromosome II reading frame ORF YBR172c
1744	11645	21513	5.5	3.2E-01	AW957194.1	EST_HUMAN	EST369264 MAGE resequences, MGD Homo sapiens cDNA
1744	11645	21514	5.5	3.2E-01	AW957194.1	EST_HUMAN	EST369264 MAGE resequences, MGD Homo sapiens cDNA
1800	11668	21574	1.16	3.2E-01	AL111655.1	NT	<i>Botrytis cinerea</i> strain T 4. gDNA library under conditions of nitrogen deprivation
2114	12003	21901	2.89	3.2E-01	BF203817.1	EST_HUMAN	601868804F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4111512 5'
2494	12368		2.9	3.2E-01	7710079	NT	Mus musculus Pbx/Knoten 1 homeobox (Pknok1), mRNA
2677	12542	22433	1.55	3.2E-01	AF060568.1	NT	Homo sapiens promyelocytic leukemia zinc finger protein (PLZF) gene, complete cds
3556	13470		0.96	3.2E-01	D10872.1	NT	Human h NAT allele 3-2 gene for arylamine N-acetyltransferase
3868	13779		0.97	3.2E-01	AL161546.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 46
4295	14193	23977	1.35	3.2E-01	M18818.1	NT	Rabbit beta-like globin gene cluster encoding the epsilon, gamma, delta (pseudogene) and beta globin polypeptides, complete cds
4375	14271	24052	0.81	3.2E-01	AF111167.2	NT	Homo sapiens jun dimerization protein gene, partial cds; cts gene, complete cds; and unknown gene
4397	14293	24077	1.33	3.2E-01	Q10268	SWISSPROT	HYPOTHETICAL 81.7 KD PROTEIN C13G7.04C IN CHROMOSOME 1 PRECURSOR
4632	14520		5.86	3.2E-01	BF693617.1	EST_HUMAN	602081972F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4216505 5'
4907	15081		1.18	3.2E-01	M32352.1	NT	Mouse renin (Ren-1-d) gene, complete cds
5133	15000	24771	0.98	3.2E-01	AY008847.1	NT	Homo sapiens interleukin 12 p40 subunit (IL12B) gene, IL12B-1 allele, complete cds
5223	15146	24913	2.82	3.2E-01	BE173984.1	EST_HUMAN	CM0-H70569-060300-269-f10 HT0569 Homo sapiens cDNA
6752	16631	26819	1.42	3.2E-01	M60266.1	NT	Rat ISO-atrial natriuretic factor gene, complete cds
6872	16751	26946	13.32	3.2E-01	X02508.1	NT	<i>H.sapiens</i> gene fragment for acetylcholine receptor (AChR) alpha subunit exons 8, 9 and 3' flanking region
6875	16754	26951	14.29	3.2E-01	BF311635.1	EST_HUMAN	601897107F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126633 5'

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6929	16807			1.35	3.2E-01 AL161574.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No 70
6986	16863	27056		1.5	3.2E-01 AE002015.1	NT	Deinococcus radiodurans R1 section 152 of 229 of the complete chromosome 1
7247	17124			2.19	3.2E-01 M86511.1	NT	Human monocyte antigen CD14 (CD14) mRNA, complete cds
7741	17591	27812		3	3.2E-01 U44914.1	NT	Borrelia burgdorferi plasmid cp32-2, espC and espD genes, complete cds; and unknown genes
7910	17760			3.25	3.2E-01 AB01399.1	NT	Homo sapiens gene for AF-6, complete cds
8058	17949	28199		2.7	3.2E-01 T06813.1	EST_HUMAN	EST04702 Fetal brain, Stratagene (cat#836206) Homo sapiens cDNA clone HFBD221
9152	19662			3.28	3.2E-01 L07288.1	NT	Drosophila melanogaster laminin A (Lam-A) mRNA, complete cds
9669	19228			2.97	3.2E-01 O83217	SWISSPROT	ELONGATION FACTOR TU (EF-TU)
9801	19313			1.58	3.2E-01 L39874.1	NT	Homo sapiens deoxyribonuclease gene, complete cds
9855	19696	24898		1.57	3.2E-01 BE385776.1	EST_HUMAN	601275480F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3616746 5'
2636	12503	22397		3.73	3.1E-01 R18051.1	EST_HUMAN	ye0106.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125051 5' similar to gb:MG4241 QM PROTEIN (HUMAN);
2665	12655	22419		3.45	3.1E-01	7661971 NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2665	12655	22420		3.45	3.1E-01	7661971 NT	Homo sapiens KIAA0174 gene product (KIAA0174), mRNA
2827	127056			1.01	3.1E-01 AW629036.1	EST_HUMAN	hi46108.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2975391 3'
3136	13061			2.78	3.1E-01 AB029069.1	NT	Mus musculus gene for Ser/Thr kinase KKLAMRE, exon 6
3832	13744	23536		1.15	3.1E-01 A1251586.1	NT	Daucus carota mRNA for transcription factor E2F (E2F gene)
5073	14943	24717		0.99	3.1E-01 AA576308.1	EST_HUMAN	nm61h05.s1 NCI_CGAP_Bi3 Homo sapiens cDNA clone IMAGE:1072761 3'
5365	15285	25119		8.66	3.1E-01 AF176111.1	NT	Homo sapiens hepatocyte nuclear factor-3 alpha (HNF3A) gene, exon 1
5447	15368			45.03	3.1E-01 Y13278.1	NT	Mus musculus mRNA for polyvinyl
5527	15444	25510		1.94	3.1E-01 AF184122.1	NT	Homo sapiens filamin 2 (FLN2) gene, exons 10 through 22
5880	15796	25918		1.34	3.1E-01 AW983549.1	EST_HUMAN	RC3-HN0001-310301-011-b074_HN0001 Homo sapiens cDNA
6160	19438	24861		2.4	3.1E-01 BE73792.1	EST_HUMAN	6013061121F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3640420 5'
7023	16900	27092		1.87	3.1E-01 R45318.1	EST_HUMAN	3g46f01.s1 Soares infant brain 1N1B Homo sapiens cDNA clone IMAGE:356399 3'
7791	17641	27874		7.76	3.1E-01 BF696639.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
7791	17641	27875		7.76	3.1E-01 BF696639.1	EST_HUMAN	602124743F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4281611 5'
7832	17682			1.96	3.1E-01 AI244001.1	EST_HUMAN	qf61e11.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1863980 3' similar to gb:S55700
8211	18095	28348		1.95	3.1E-01 BF216117.1	EST_HUMAN	HYDROXYMETHYL GLUTARYL-COA LYASE PRECURSOR (HUMAN);
8823	18636	28920		1.99	3.1E-01	7662291 NT	601883592F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095814 5'
9279	18982			1.63	3.1E-01 AF294308.1	NT	Anolis opalinus isolate CS NADH dehydrogenase subunit 2 (ND2) gene, complete cds; mitochondrial gene for mitochondrial product
9315	19007			1.64	3.1E-01 AF304162.1	NT	Stizostedion vitreum 40S ribosomal protein S11 mRNA, partial cds
9457	19089			2.45	3.1E-01 AF195953.1	NT	Homo sapiens membrane-bound aminopeptidase P (ANPEP2) gene, complete cds

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9806	19318			3.11	3.1E-01 AF196779.1	NT	Homo sapiens transcription factor IGHM enhancer 3, JM11 protein, JM4 protein, JM5 protein, T54 protein, JM10 protein, A4 differentiation-dependent protein, triple LIM domain protein 6, and synaptophysin genes, complete cds; and L-type calcium channel $\alpha 2$
66	12655	19866		1.58	3.0E-01 67550831	NT	Mus musculus protein kinase C, epsilon (PKce), mRNA
254	10220	20037		11.12	3.0E-01 A1271735.1	NT	Homo sapiens Xq pseudautosomal region; segment 1/2
1204	11114	209860		1.89	3.0E-01 AW30400.1	EST_HUMAN	xS6308.x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2774343 3'
1491	11396	21256		6.26	3.0E-01 AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
2089	11978	21873		0.86	3.0E-01 AF237778.1	NT	Rattus norvegicus Ca2+/calmodulin-dependent protein kinase II, alpha subunit mRNA, 3' untranslated region
3175	13100			0.98	3.0E-01 AB030481.1	NT	Corynebacterium sp. ALY-1 alpPG gene for polyglucuronate lyase, complete cds
3789	13701	23488		1.34	3.0E-01 AW817785.1	EST_HUMAN	PM1-ST0262-261199-00-1-901 ST0262 Homo sapiens cDNA
4412	14306	24039		1.91	3.0E-01 AJ006755.1	NT	Balaenoptera physalus gene encoding atrial natriuretic peptide
5283	15205	24981		5.34	3.0E-01 BE741629.1	EST_HUMAN	6015949860F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3948734 5'
5379	15298	25147		3.18	3.0E-01 BE693575.1	EST_HUMAN	RC3-BT0333-180700-11-a03 B10333 Homo sapiens cDNA
5379	15298	25148		3.18	3.0E-01 BE693575.1	EST_HUMAN	RC3-BT0333-180700-11-a03 B10333 Homo sapiens cDNA
5401	15320	25368		3.51	3.0E-01 U01247.1	NT	Mus musculus 129/sv Clara cell 10 kDa protein (mCC10) gene, complete cds
6036	16031	26171		2.61	3.0E-01 D16313.1	NT	Mouse cytokeratin 15 gene, complete cds
6335	16198	26353		2.57	3.0E-01 10947007	NT	Mus musculus midolloin (Midn-pending), mRNA
6429	16280	26451		1.35	3.0E-01 AF071810.1	NT	Streptococcus pneumoniae strain DB15 RspA (pspA) gene, partial cds
6625	16505	26633		1.25	3.0E-01 AE001755.1	NT	Thermatoga maritima section 67 of 136 of the complete genome
6877	16756			4.67	3.0E-01 9910161	NT	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (Clec59), mRNA
6937	16815	27007		1.27	3.0E-01 BE66083.1	EST_HUMAN	601339079F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3681594 5'
7944	17794	28034		1.89	3.0E-01 AB030231.1	NT	Aspergillus oryzae bipA gene for ER chaperone BiP, complete cds
8880	18785	29074		2.89	3.0E-01 H51029.1	EST_HUMAN	yp84b10.r1 Seacrest fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:194107 5'
8980	18785	29075		2.89	3.0E-01 H51029.1	EST_HUMAN	yp84b10.r1 Seacrest fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:194107 5'
9564	19647			1.43	3.0E-01 A1297631.1	NT	Rattus norvegicus mRNA for glyceraledehyde-3-phosphate dehydrogenase type 2 (gapdh-2 gene)
9836	19690			2.76	3.0E-01 6677766	NT	Mus musculus ribose 5-phosphate isomerase A (Rpl4), mRNA
1978	11871	21762		1.6	2.9E-01 AE001736.1	NT	Aquifex aeolicus section 68 of 109 of the complete genome
2201	12088	21989		0.99	2.9E-01 AF222718.1	NT	Chrysosodidymus synuroideus mitochondrion, complete genome
3147	13072	22873		1.03	2.9E-01 AF078111.1	NT	Xenopus laevis transcription factor E2F mRNA, complete cds
3213	13137	22949		2.29	2.9E-01 AW754239.1	EST_HUMAN	PM1-CT0326-171299-00-1-f12 CT0326 Homo sapiens cDNA
3213	13137	22940		2.29	2.9E-01 AW754239.1	EST_HUMAN	PM1-CT0326-171299-00-1-f12 CT0326 Homo sapiens cDNA

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3821	13733	23522	1.28	2.9E-01	AI610836.1	EST_HUMAN	tp21at1x1 NCL_CGAP_Gas4 Homo sapiens cDNA clone MAGE:218841 2'3' similar to gb D15050 NIL-2A
3994	13901		0.82	2.9E-01	AW002902.1	EST_HUMAN	ZINC FINGER PROTEIN (HUMAN); contains element L1 repetitive element;
4384	14280	24059	1.01	2.9E-01	AA284468.1	EST_HUMAN	wr02f10x1 NCL_CGAP_GC6 Homo sapiens cDNA clone MAGE:2480395 3'
4388	14284	24064	0.78	2.9E-01	AF+34119.1	NT	zs57d12r1 NCL_CGAP_GCB1 Homo sapiens cDNA clone MAGE:701591 5' similar to contains Alu repetitive element;
4388	14284	24065	0.78	2.9E-01	AF+34119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
4729	14615	24401	0.92	2.9E-01	AB019029.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
5218	15141		1.49	2.9E-01	R37485.1	EST_HUMAN	Mus musculus gene, complete cds, similar to EVLM1
5522	15440	25504	4.45	2.9E-01	X66098.1	NT	yf77er12.s1 Soares infant brain 1NIB Homo sapiens cDNA clone MAGE:28291 3'
5522	15440	25505	4.45	2.9E-01	X66098.1	NT	B.subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16, 18, 28, 30 and levanase
5529	15448	25513	5.83	2.9E-01	6679682	NT	B.subtilis levanase operon levD, levE, levF, levG and sacC (partial) genes for fructose phosphotransferase system polypeptides P16, 18, 28, 30 and levanase
5818	15724	25838	2.24	2.9E-01	U03420.1	NT	Mus musculus Eph receptor A8 (Ephag8), mRNA
6171	15128	24847	1.51	2.9E-01	AF+42329.1	NT	Bos taurus myosin I mRNA, complete cds
6218	16084	26234	2.52	2.9E-01	Q03389	SWISSPROT	Mus musculus Filh protein (Filh) gene, complete cds; and Ligh protein (Ligh) gene, partial cds
6249	16115	26267	1.74	2.9E-01	AF+100956.1	NT	PUTATIVE MULTICOPPER OXIDASE YDR506C
6619	16489	26686	1.76	2.9E-01	BEE40422.1	EST_HUMAN	Mus musculus major histocompatibility locus class I region; Fas-binding protein Daxx (Daxx) gene, partial cds; Bng1 (BNG1), tapasin (tapasin), RatGDS-like factor (RLF), KE2 (KE2), BING4 (BNG4), beta1, 3-galactosyl transferase (beta1,3-galactosyl tr-> galactosyl)
6619	16489	26687	1.76	2.9E-01	BEE40422.1	EST_HUMAN	601065530f1 NIH_MGC_10 Homo sapiens cDNA clone MAGE:3452287 5'
8267	18147	28387	1.96	2.9E-01	AF+8843.1	NT	601065530f1 NIH_MGC_10 Homo sapiens cDNA clone MAGE:3452287 5'
8502	18375	28639	2.69	2.9E-01	V01394.1	NT	Trypanosoma cruzi stage-specific surface glycoprotein gp82 (gp82) mRNA, partial cds
8502	18375	28640	2.69	2.9E-01	V01394.1	NT	Torpedo californica mRNA encoding acetylcholine receptor gamma subunit
8864	18676	28965	1.77	2.9E-01	AA935373.1	EST_HUMAN	ny35h02.s1 NCL_CGAP_Pr12 Homo sapiens cDNA clone MAGE:1273779 similar to contains LTR8.12 LTR8 repetitive element;
8866	18678	28967	4.54	2.9E-01	AL139078.2	NT	Campylobacter jejuni NGTC11168 complete genome, segment 5/6
9514	19127	25260	1.53	2.9E-01	AW005674.1	EST_HUMAN	wz28sf05.x1 NCL_CGAP_Bm25 Homo sapiens cDNA clone MAGE:2565921 3' similar to contains element MER29 repetitive element;
9602	19184	25248	2.74	2.9E-01	AF092453.1	NT	Homo sapiens TNF- α -inducible RNA binding protein (TIRP) gene, complete cds
9644	19212		1.33	2.9E-01	BE78199.1	EST_HUMAN	601482059f1 NIH_MGC_68 Homo sapiens cDNA clone MAGE:3884559 5'
9883	19367	25188	4.86	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus
9883	19367	25189	4.86	2.9E-01	Y08937.1	NT	Chlamydomonas reinhardtii mRNA for nitrite reductase structural locus

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556	10497			1.84	2.8E-01 U67136.1	NT	Rattus norvegicus A kinase anchoring protein AKAP150 mRNA, complete cds
1067	10983	20828		2.47	2.8E-01 AF168050.1	NT	Guita guira oocyte maturation factor Mos (c-mos) gene, partial cds
1256	11163	21013		1.1	2.8E-01 BE313442.1	EST_HUMAN	6011148733F1 NIH_MGGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1256	11163	21014		1.1	2.8E-01 BE313442.1	EST_HUMAN	6011148733F1 NIH_MGGC_19 Homo sapiens cDNA clone IMAGE:3163688 5'
1269	11176	21025		1.01	2.8E-01 D86550.1	NT	Human mRNA for serine/threonine protein kinase, complete cds
1698	11598	21470		1.55	2.8E-01 AW380020.1	EST_HUMAN	QV1-CT3364-120200-065-b05 CT3364 Homo sapiens cDNA clone DKFZp586l2321
1986	11860	21750		1.77	2.8E-01 AL047620.1	EST_HUMAN	DKFZp586l2321_1' 586 (synonym: hute1) Homo sapiens cDNA clone IMAGE:2912333 3'
2084	11974	21869		1.47	2.8E-01 AW351195.1	EST_HUMAN	hg44b03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2912333 3'
2423	12300	22197		2.94	2.8E-01 AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2423	12300	22198		2.94	2.8E-01 AE000494.1	NT	Escherichia coli K-12 MG1655 section 384 of 400 of the complete genome
2500	12375			2.47	2.8E-01 AL161565.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65
2630	12498	22388		1.37	2.8E-01 AB020975.1	NT	Arabidopsis thaliana mRNA for lipoyltransferase, complete cds
2840	12867			1.49	2.8E-01 AF179480.1	NT	Toxoplasma gondii 90kDa heat-shock protein (HSP90) mRNA, partial cds
2841	12868	22667		2.48	2.8E-01 Z14037.1	NT	B.taurus microsatellite (ETH121)
2941	12868	22668		2.48	2.8E-01 Z14037.1	NT	B.taurus microsatellite (ETH121)
3332	13252	23057		1.1	2.8E-01 AF000004.1	NT	Pyrococcus horikoshii OT3 genomic DNA_777001-894000 nt. position (4/7)
3915	13824	23604		1.75	2.8E-01 AE001180.1	NT	Borrelia burgdorferi (section 66 of 70) of the complete genome
4103	14003			2.21	2.8E-01 A1090868.1	EST_HUMAN	ov44g10.x1 Soares_nestis_NHT Homo sapiens cDNA clone IMAGE:1640226 3' similar to contains Alu repetitive element contains element MER22 repetitive element;
4352	14248	24034		0.98	2.8E-01 AL021127.2	NT	Mus musculus chromosome X contigA; putative Mage8 gene, Caltratin, NAD(P) steroid dehydrogenase and Zinc finger protein 185
4357	14253	24038		2.2	2.8E-01 P13615	SWISSPROT	RNA POLYMERASE BETA SUBUNIT (LARGE STRUCTURAL PROTEIN) (L PROTEIN)
4673	14559	24352		1.03	2.8E-01 D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4673	14559	24353		1.03	2.8E-01 D15050.1	NT	Human mRNA for transcription factor AREB6, complete cds
4722	14608	24394		2.8	2.8E-01 AF030154.1	NT	Bovine adenovirus 3 complete genome
4755	14640	24427		1.54	2.8E-01 BF528188.1	EST_HUMAN	602042601F1_NCI_CGAP_Bm67_Homo sapiens cDNA clone IMAGE:4180129 5'
4787	14672	24459		1.7	2.8E-01 A1272689.1	EST_HUMAN	q153c11.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1876628 3' similar to contains Alu repetitive element contains element LTR5 repetitive element;
5252	19440	24948		21.36	2.8E-01 AA349997.1	EST_HUMAN	EST57072 Infant brain Homo sapiens cDNA 5' end
5443	15363	25419		2.33	2.8E-01 AB016625.1	NT	Homo sapiens OCTN2 gene, complete cds
5770	15677	25784		1.44	2.8E-01 AF03124.1	NT	Mesembryanthemum crystallinum fructose-biphosphate aldolase mRNA, complete cds
5770	15677	25785		1.44	2.8E-01 AF03124.1	NT	Mesembryanthemum crystallinum fructose-biphosphate aldolase mRNA clone IMAGE:3085182 3'
6038	15941	26073		7.67	2.8E-01 BF511215.1	EST_HUMAN	U1-H-B14-acid-04-U1s1 NCI_CGAP_Sub8 Homo sapiens cDNA clone IMAGE:3085182 3'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6713	16593	26781	1.24	2.8E-01	AI346126.1	EST_HUMAN	qp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1
6713	16593	26782	1.24	2.8E-01	AI346126.1	EST_HUMAN	qp48h01.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1926289 3' similar to gb:X06323_cds1
6778	16657	26847	2.39	2.8E-01	U51688.1	NT	Homo sapiens lanosterol 14-alpha demethylase cytochrome P450 (CYP51) gene, exon 5
6994	16871		7.25	2.8E-01	BF347847.1	EST_HUMAN	6022029877F NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4158525 5'
7311	17187	27398	1.35	2.8E-01	AF080592.1	NT	Mus musculus centrin (Cetn2) gene, complete cds
7600	17451		1.15	2.8E-01	L13654.1	NT	Lyopersicon esculentum peroxidase (TPX1) mRNA, complete cds
7789	17639	27872	2.79	2.8E-01	7706163	NT	Homo sapiens hypothetical protein (LOC51319) mRNA
8126	18014	28261	2.27	2.8E-01	BF241062.1	EST_HUMAN	601880794F NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
8126	18014	28262	2.27	2.8E-01	BF241062.1	EST_HUMAN	601880794F NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4109350 5'
8153	18041	28291	3.01	2.8E-01	BF095970.1	EST_HUMAN	601852148F NIH_MGC_56 Homo sapiens cDNA clone IMAGE:407626 5'
8254	18134	28352	2.62	2.8E-01	AF051662.1	NT	Drosophila heteroneura fruitless (fru) gene, alternative splice products, 5' flanking region, exons 1 through 7 and complete cds
8359	18466		3.49	2.8E-01	BF074023.1	EST_HUMAN	6021317418F NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4273853 5'
9552	19750		6.37	2.8E-01	DS3329.1	NT	Mus musculus DNA for prostaglandin D2 synthase, complete cds
9657	19219	25236	3.11	2.8E-01	BE778589.1	EST_HUMAN	PM4-HT0606-03040-001-a07 HT0606 Homo sapiens cDNA
9826	19851		1.69	2.8E-01	11433629	NT	Homo sapiens CDC42-binding protein kinase beta (DMPK-like) (CDC42BP), mRNA
468	10411	20230	2.33	2.7E-01	Y17324.1	NT	Rattus norvegicus CDK104 mRNA
597	10533	20341	3.14	2.7E-01	AA450061.1	EST_HUMAN	239b10 s1 Scores_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:783827 3' similar to contains Alu repetitive element;
1240	11147	20956	1.49	2.7E-01	AB004906.1	NT	Ipomoea purpurea transposable element Tip00 gene for transposase, complete cds
1604	11509		1.73	2.7E-01	X79815.1	NT	G.lambla SR2 gene
1698	11600	21471	2.96	2.7E-01	W58067.1	EST_HUMAN	z022h10.r1 Scores_fetal_heart_NBHH19W Homo sapiens cDNA clone IMAGE:341443 5'
1738	11639	21507	1.25	2.7E-01	IP03341	SWISSPROT	GAG POLYPROTEIN [CONTAINS: INNER COAT PROTEIN P12; CORE PROTEIN P15; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10]
2088	12712		2.38	2.7E-01	AF047575.1	NT	Rattus norvegicus vesicular monoamine transporter type 2, promoter region and exon 1
2316	12497	22094	8.78	2.7E-01	Y1388.1	EST_HUMAN	ta43c11.x2 NCI_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2046836 3' similar to contains element L1 repetitive element;
2406	12283	22180	3.51	2.7E-01	AI310858.1	EST_HUMAN	CM1-HT0875-060900-385-e05 HT0875 Homo sapiens cDNA
2956	12883		1.25	2.7E-01	BF08284.1	EST_HUMAN	CM1-HT0875-060900-385-e05 HT0875 Homo sapiens cDNA
3929	13838	23618	1.88	2.7E-01	AI928015.1	EST_HUMAN	ws022e11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2462828 3'
3943	13851	23626	2.31	2.7E-01	L77569.1	NT	Homo sapiens DiGeorge syndrome critical region, telomeric end
4796	14681	24498	0.89	2.7E-01	L27516.1	NT	Triticum aestivum (Wcs6) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4973	14848			3.5	2.7E-01 AW856131.1	EST_HUMAN	RC1-CT0286-230200-016-e03 CT0286 Homo sapiens cDNA
5221	15144	24838		3.49	2.7E-01 P17277	SWISSPROT	HOMEobox PROTEIN HOXA4 (CH10X-1.4)
6064	16047	26192		2.25	2.7E-01 Q6f554	SWISSPROT	FIBRILLIN 1 PRECURSOR
6527	16386	26565		2.23	2.7E-01 AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
6527	16386	26566		2.23	2.7E-01 AF248054.1	NT	Bos taurus micromolar calcium activated neutral protease 1 (CAPN1) gene, exons 11-20, and partial cds
7378	17247	27453		10.08	2.7E-01 O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRRS)
7378	17247	27454		10.08	2.7E-01 O83809	SWISSPROT	THREONYL-TRNA SYNTHETASE (THREONINE-TRNA LIGASE) (THRRRS)
7379	17248			2.24	2.7E-01 P37928	SWISSPROT	FIMBRIAE W PROTEIN
7801	17651	27888		1.29	2.7E-01 AF091848.1	NT	Oryctolagus cuniculus calgranulin C mRNA, partial cds
7827	17677	27921		1.93	2.7E-01 AF087434.1	NT	Mus musculus transcription factor NF-ATc isoform a (NF-ATc) mRNA, complete cds
8187	18073	28322		1.76	2.7E-01 AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADDBC0005 5'
8187	18073	28323		1.76	2.7E-01 AV705043.1	EST_HUMAN	AV705043 ADB Homo sapiens cDNA clone ADDBC0005 5'
8197	18082	28333		4.09	2.7E-01 AJ133269.1	NT	Homo sapiens cavinlin-1/2 locus, Contig1, D7S522, genes CAV2 (exons 1, 2a, and 2b), CAV1 (exons 1 and 2)
9336	19034			1.27	2.7E-01 X95267.1	NT	G. gallus mRNA for nandrolone receptor type 3
9810	19320			2.15	2.7E-01 AF217491.1	NT	Homo sapiens fragile 6D oxidoreductase (FOR) gene, exon 6
462	12967	20224		1.54	2.6E-01 P78411	SWISSPROT	IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-2
472	10416			1.39	2.6E-01 D16459.1	NT	Bos taurus mRNA for mb-1, complete cds
1371	11277	21133		2.23	2.6E-01 BE885087.1	EST_HUMAN	601510838F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912345 5'
1418	11324	21188		0.97	2.6E-01 AB013290.1	NT	Glycine max pseudogene for Bd 30K
1854	11750	21624		8.59	2.6E-01 AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, config fragment No. 2
1854	11750	21625		8.59	2.6E-01 AL161472.2	NT	Arabidopsis thaliana DNA chromosome 4, config fragment No. 2
2046	11937			9.9	2.6E-01 AW733152.1	EST_HUMAN	bb04d10.x1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:2958451 3' similar to gb:NM36072 60S RIBOSOMAL PROTEIN L17A (HUMAN); gb:M14689_cds1 Mouse surflet locus surflet 3 protein gene (MOUSE);
2106	11995	21805		1.2	2.6E-01 M11844.1	NT	Human prealbumin gene, complete cds
2424	12301			2.68	2.6E-01 Y112986.1	NT	B. maritimus rbcL gene
2499	12374			9.68	2.6E-01 BE272440.1	EST_HUMAN	601126016F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:29800043 5'
3053	12980			1.03	2.6E-01 AW974531.1	EST_HUMAN	EST386655 IMAGE resequences, MAGM Homo sapiens cDNA
3485	13401			0.94	2.6E-01 BE217816.1	EST_HUMAN	h30c02.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3174914 3' similar to contains L1.13 L1 repetitive element;
3532	13448	23245		1.12	2.6E-01 M22342.1	NT	Bacteriophage T2 DNA-(adenine-N6)methyltransferase (dam) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3591	13505	23295	1.7	2.6E-01	AF229118.1	NT	Homo sapiens acetylcholinesterase collagen-like tail subunit (COLQ) gene, exons 1A, 2, 3, 4, and 5
3651	13565	23351	0.9	2.6E-01	AB017446.1	NT	Rattus norvegicus mRNA for organic anion transporter 3, complete cds
4010	13916	23691	1	2.6E-01	AW089510.1	EST_HUMAN	EST371580 MAGE sequences, MAGF Homo sapiens cDNA
4062	13984	23712	13.13	2.6E-01	BE080598.1	EST_HUMAN	QV1-BT0680-040400-132-e03 BT0630 Homo sapiens cDNA
4259	14158	23935	0.95	2.6E-01	AF175293.1	NT	Enterococcus faecium strain N97-330 vanD glycopeptide resistance gene cluster, complete cds; and unknown gene
4393	14289	24072	0.84	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4393	14289	24073	0.84	2.6E-01	AB021180.1	NT	Gallus gallus mRNA for skeletal myosin heavy chain, complete cds
4448	14342	24134	1.17	2.6E-01	AA457617.1	EST_HUMAN	aa99d07.1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:338477'5'
4548	14441	24224	1.63	2.6E-01	U01103.1	NT	Arabidopsis thaliana PSI type III chlorophyll a/b-binding protein (Lcnc31') mRNA, complete cds
4616	14504	24292	1.28	2.6E-01	AF142703.1	NT	Orphelia radicosa maturase-like protein (matK) gene, complete cds; chloroplast gene for chloroplast product
4896	14776	24554	3.56	2.6E-01	HO4858.1	EST_HUMAN	jj51e05.1r1 Soares placentae Nb2HP Homo sapiens cDNA clone IMAGE:152288'5'
5051	14923	24636	0.86	2.6E-01	PO8503	SWISSPROT	ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC, MITOCHONDRIAL PRECURSOR (MCAD)
5700	19764		2.03	2.6E-01	AE01811.1	NT	Thermotoga maritima section 123 of 136 of the complete genome
5763	15670	25777	1.93	2.6E-01	AI582557.1	EST_HUMAN	ts02e12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1; contains element LTR1 repetitive element;
5763	15670	25778	1.93	2.6E-01	AI582557.1	EST_HUMAN	ts02e12.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2227438 3' similar to SW:NDF1_RAT Q64289 NEUROGENIC DIFFERENTIATION FACTOR 1; contains element LTR1 repetitive element;
6552	16410	26588	1.52	2.6E-01	RI10365.1	EST_HUMAN	jy37a03.s1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:129004'3' similar to gb:X12517 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (HUMAN);
6585	16465	26656	1.27	2.6E-01	RI02411.1	EST_HUMAN	je82a07.r1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:124212'5'
6852	16731	26925	3.01	2.6E-01	BF343588.1	EST_HUMAN	602014422F1 NCI_CGAP_Bm64 Homo sapiens cDNA clone IMAGE:4150356'5'
6900	16779	26973	2.04	2.6E-01	Q10199	SWISSPROT	HYPOTHETICAL 75.2 KD PROTEIN C11C11.02 IN CHROMOSOME II
7046	16923	27112	4.34	2.6E-01	BE830539.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
7046	16923	27113	4.34	2.6E-01	BE830539.1	EST_HUMAN	RC5-ET0082-310500-021-F10 ET0082 Homo sapiens cDNA
7854	17704		1.16	2.6E-01	Q28295	SWISSPROT	VON WILLEBRAND FACTOR PRECURSOR (VWF)
8812	18625		93.65	2.6E-01	X51755.1	NT	Human lambda-immunoglobulin constant region complex (germline)
9136	18892		1.98	2.6E-01	10190655	NT	Mus musculus jerky (Jrk) mRNA
9328	19655		1.92	2.6E-01	BE83491.1	EST_HUMAN	60151102F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912612'5'
9395	19053	25309	2.6	2.6E-01	AF316598.1	NT	Homo sapiens NalK-ATPase gamma subunit (FXD2) gene, complete cds, alternatively spliced

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Probe SEQ ID	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9833	19333			6.03	2.6E-01 AF41325.2	NT	Homo sapiens inositol polyphosphate 1-phosphatase (INPP1) gene, complete cds
9889	19376			1.5	2.6E-01 Q01631	SWISSPROT	ADENYLYATE CYCLASE (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE)
241	10209	20025		2.12	2.5E-01	4502296 NT	Homo sapiens ATP synthase, H ⁺ transporting, mitochondrial F ₁ complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
242	10209	20025		1.86	2.6E-01	4502296 NT	Homo sapiens ATP synthase, H ⁺ transporting, mitochondrial F ₁ complex, delta subunit (ATP5D), nuclear gene encoding mitochondrial protein, mRNA
255	10221			3.24	2.6E-01 M26501.1	NT	Starfish (<i>P. ochraceus</i>) cytoplasmic actin gene, complete cds
815	10743	20589		1.32	2.5E-01 U09964.1	NT	Mus musculus ICR/Swiss glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
1044	10962			1.86	2.5E-01 AE002156.1	NT	Ureaplasma urealyticum section 57 of 59 of the complete genome
1105	11021	20864		9.5	2.5E-01 T89837.1	EST_HUMAN	ye11g07.1 Strategene lung (#837210) Homo sapiens cDNA clone IMAGE:1174685'
1503	11407	21296		0.85	2.5E-01 AL115624.1	NT	Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1697	11599			5.43	2.5E-01	4885406 NT	Homo sapiens hyperpolarization activated cyclic nucleotide-gated potassium channel 4 (HCN4) mRNA
1840	12706	21612		0.88	2.5E-01 BEC96604.1	EST_HUMAN	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA
1840	12706	21613		0.88	2.5E-01 BEC96604.1	EST_HUMAN	PM4-CT0400-310700-005-d08 CT0400 Homo sapiens cDNA
2357	12237			8.29	2.5E-01 AE000675.1	NT	Aquifex aeolicus section 7 of 109 of the complete genome
2446	12323			1.35	2.5E-01 AA251987.1	EST_HUMAN	zst1af2.1 NCL CGAP GCB1 Homo sapiens cDNA clone IMAGE:6848625'
2597	12466	22359		0.97	2.5E-01 X95310.1	NT	B. tauri mRNA for D-aspartate oxidase
3336	13285			2.87	2.5E-01 AW913471.1	EST_HUMAN	EST385464 MAGE sequences, MAGE Homo sapiens cDNA
3480	13406	23211		0.86	2.5E-01 AF233875.1	NT	Danio rerio peptide YY precursor gene, complete cds
3502	13419	23220		7.93	2.5E-01 AL161717.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 29
3774	13986	23468		1.15	2.5E-01 AI741483.1	EST_HUMAN	wg11c07_x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:23647803'
3774	13986	23469		1.15	2.5E-01 AI741483.1	EST_HUMAN	wg11c07_x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:23647803'
3977	13984			0.83	2.5E-01 P522323	SWISSPROT	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR
4222	14120			1.2	2.5E-01 Q03314	SWISSPROT	RHB PROTEIN
4514	14407	24193		0.96	2.5E-01 AF242431.1	NT	Mus musculus neuronal apoptosis inhibitory protein 6 (Nrip6) gene, complete cds; and Nrip3 gene, exons 2-9 and 11-16
4643	14531			1.14	2.5E-01 Q27225	SWISSPROT	MOLT-INHIBITING HORMONE PRECURSOR (MTH)
4649	14535	24324		3.78	2.5E-01 AF007768.1	NT	Chorisoneura fumiferana diapause associated protein 2 (DAP2) mRNA, complete cds
4672	14558	24351		2.19	2.5E-01 AE004416.1	NT	Vibrio cholerae chromosome II, section 73 of 93 of the complete chromosome
4698	14584			3.16	2.5E-01 AJ23013.1	NT	Mus musculus annexin V gene, intron 4 segment containing 5'LTR and gag portion of MuERV-L (murine endogenous retrovirus) element
4726	14612	24398		0.79	2.5E-01 BE896785.1	EST_HUMAN	601437468F_NIH_MGC_72 Homo sapiens cDNA clone IMAGE:39226005'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4750	14635	24421	0.89	2.5E-01	AB011070.1	NT	Mus musculus gene for uncoupling protein 3, 5'-flanking region and partial 5'UTR hh7509.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:29688649 5' similar to contains TAR1.t2
5169	15035	24802	0.86	2.5E-01	AW663183.1	EST_HUMAN	TAR1 repetitive element; hh7509.y1 NCI_CGAP_GU1 Homo sapiens cDNA clone IMAGE:29688649 5' similar to contains TAR1.t2
5169	15035	24803	0.86	2.5E-01	AW663183.1	EST_HUMAN	TAR1 repetitive element;
5264	15186	24962	11.62	2.5E-01	S83390.1	NT	T3 receptor-associating cofactor-1 [Human, fetal liver, mRNA, 2930 nt]
6366	16229		1.32	2.5E-01	AF134119.1	NT	Mus musculus SKD1 (Skd1) gene, complete cds
6500	16359	26532	3.73	2.5E-01	AL163282.2	NT	Homo sapiens chromosome 21 segment HS21C082
6583	16463	26655	2.99	2.5E-01	BF109040.1	EST_HUMAN	7157a03.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone IMAGE:3523589 3'
6788	16667	26858	2.25	2.5E-01	BF038595.1	EST_HUMAN	60145923851 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3862809 5'
7020	16897	27087	3.95	2.5E-01	H53226.1	EST_HUMAN	yq84f07.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:202501 5'
7481	17351	27554	16.11	2.5E-01	U89661.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
7481	17351	27555	16.11	2.5E-01	U89661.2	NT	Homo sapiens matrix metalloproteinase MMP Rasi-1 gene, promoter region
7522	17341	27547	2.04	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, Partial cds
7522	17341	27548	2.04	2.5E-01	AF085164.1	NT	Hordeum vulgare receptor-like kinase LRK10 gene, Partial cds
7814	17664	27904	1.5	2.5E-01	AW1581987.1	EST_HUMAN	RC3-ST0186-130100-01-a07 ST0186 Homo sapiens cDNA
8010	17860	28105	1.62	2.5E-01	AW1522246.1	EST_HUMAN	xg40c10.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2630034 3' similar to contains Alu repetitive element; contains element MSR1 repetitive element;
8011	17861	28106	1.68	2.5E-01	X58491.1	NT	Mouse L1Md LINE DNA
8426	18300	28556	2.32	2.5E-01	D50914.1	NT	Human mRNA for KIAA0124 gene, partial cds
9074	18851	29117	2.45	2.5E-01	AF200528.1	NT	Zea mays cellulose synthase-4 (CesA4) mRNA, complete cds
9100	19729		4.2	2.5E-01	AL161541.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 41
9559	19581	25072	1.28	2.5E-01	AF170072.1	NT	Spodoptera frugiperda CALNUC mRNA, complete cds
541	10482	20292	1.53	2.4E-01	AA938316.1	EST_HUMAN	on7004.51 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1562023 3'
830	10757	20608	2.38	2.4E-01	BF576124.1	EST_HUMAN	602132442F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271578 5'
1282	11190	21041	17.41	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1282	11190	21042	17.41	2.4E-01	AJ289880.1	NT	Homo sapiens KIAA0851 gene (partial), XT3 gene and LZTFL1 gene
1362	11268	21123	1.04	2.4E-01	Y17293.1	NT	Homo sapiens FL-1 gene, partial
1808	11705		24.08	2.4E-01	AF267753.1	NT	Mesembryanthemum crystallinum putative potassium channel protein Mkt1p mRNA, complete cds
1858	11754	21629	1.41	2.4E-01	AF255708.1	NT	Zacccys dhumannades fructose-1,6-bisphosphatase mRNA, complete cds
2091	11980	21875	0.88	2.4E-01	AF111168.2	NT	Homo sapiens serine palmitoyl transferase, subunit II gene, complete cds; and unknown genes
2122	12010		1.16	2.4E-01	R45384	SWISSPROT	IMMUNOGLOBULIN A1 PROTEASE PRECURSOR (IGA1 PROTEASE)
2215	12101	22005	2.01	2.4E-01	AE000680.1	NT	Aquifex aeolicus section 12 of 109 of the complete genome

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Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2332	12213	22111	0.85	2.4E-01	BF002171.1	EST_HUMAN	7h23d04.x1 NCI_CGAP_Cof6 Homo sapiens cDNA clone IMAGE:3316807 3' similar to SW:PRSB_XEN1A
2491	12366	22260	1.63	2.4E-01	Z36534.1	NT	O42586 26S PROTEASE REGULATORY SUBUNIT 6A ; D.discoidinum (A33-K) ponA gene
2784	12396	22491	2.14	2.4E-01	X71753.1	NT	S.pombe swif gene
2756	12618	22510	6.68	2.4E-01	AF030154.1	NT	Bovine adenovirus 3 complete genome
3093	13020		2.82	2.4E-01	U72726.1	NT	Oryza longistaminata receptor kinase-like protein, family member D, and retrofit (gag/pol) genes, complete cds
3109	13035	22831	1.85	2.4E-01	X74298.1	NT	H.sapiens AGT gene, PstI fragment of intron 4
4817	14700	24486	0.88	2.4E-01	BE160080.1	EST_HUMAN	QV1-HT0412-02040-0136-b10 HT0412-Homo sapiens cDNA
4981	14856	24622	50.15	2.4E-01	D00944.1	NT	Hepatitis C virus genomic RNA for polyprotein, complete cds
5469	15389	25451	7.53	2.4E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
5469	15389	25452	7.53	2.4E-01	AF091216.1	NT	Mus musculus Wm protein (Wm) gene, complete cds
5563	15558	25583	2.13	2.4E-01	BF592386.1	EST_HUMAN	7f54d04.x1 NCI_CGAP_Br16 Homo sapiens cDNA clone IMAGE:333503 3' similar to SW:SFR4_HUMAN
5642	15555	25648	2.66	2.4E-01	AF035546.1	NT	Q08170 SPlicing FACTOR, ARGININE/SERINE-RICH 4 ; contains element TAR1 TAR1 repetitive element
5705	15613	25714	2.16	2.4E-01	7661801	NT	Drosophila melanogaster p38a MAP kinase gene, complete cds
5937	15842	25966	1.79	2.4E-01	AI698989.1	EST_HUMAN	wc62c11.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2323220 3' similar to dbJ03464
6345	16208	26371	8.87	2.4E-01	U43001.1	NT	PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (HUMAN); Bos taurus guanylyl cyclase-activating protein 2 (Gua2) mRNA, complete cds
6880	16739	26931	1.62	2.4E-01	AI012585.1	NT	Tetrahymena thermophila macronuclear gene encoding ribosomal protein L3, exons 1-2
7517	17305	27511	5.72	2.4E-01	AI693515.1	EST_HUMAN	wd43e02.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2330906 3' similar to contains MER22_b1 TAR1 repetitive element ;
7965	17815	28056	1.93	2.4E-01	Q03692	SWISSPROT	COLLAGEN ALPHA 1(X) CHAIN PRECURSOR
8149	18037	28285	3.63	2.4E-01	AL161494.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 6
8209	18093	28347	1.99	2.4E-01	AF030199.1	NT	Mus musculus type 1 sigma receptor gene, complete cds
8554	18406		2.42	2.4E-01	Z21647.1	NT	P.asterica mosaic virus genomic RNA
9030	18921	29109	1.55	2.4E-01	AE217491.1	NT	Homo sapiens fragile XID oxidoreductase (FOR) gene, exon 6
9162	19526		2.39	2.4E-01	AF04213.1	NT	Arabidopsis thaliana ethylene-insensitive3-like1 (EIL1) mRNA, complete cds
9222	18945		2.54	2.4E-01	AJ278191.1	NT	Mus musculus mRNA for putative mc7 protein (mc7 gene)
9439	19509		1.59	2.4E-01	VO1507.1	NT	Galus gallus gene coding for a-actin
9650	19746		1.26	2.4E-01	BF229975.1	EST_HUMAN	RC3-CT0413-100800-023-b06 CT0413 Homo sapiens cDNA
9865	19355		3.35	2.4E-01	AL163281.2	NT	Homo sapiens chromosome 21 segment HS21C081
333	10330	20153	0.9	2.3E-01	ST5898.1	NT	aromatase [P]oephila guttata=zebra finches, ovary, mRNA, 3188 nt

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 Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
621	10558			4.42 -	2.3E-01 U39713.1	NT	Mycoplasma genitalium section 35 of 51 of the complete genome
651	10587	20403		19.84	2.3E-01 U67596.1	NT	Methanococcus jannaschii section 138 of 150 of the complete genome
918	10842	20687		3.35	2.3E-01 BE11983.1	EST_HUMAN	601142073F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:3505818 5'
1494	11398	21298		1.5	2.3E-01 6677980	NT	Mus musculus vacuolar protein sorting 4b (yeast) (Yps4b), mRNA
1546	11451			0.88	2.3E-01 U22837.2	NT	Yersinia pestis HmsH (HmsF), HmsR (hmsR), and HmsS (hmsS) genes, complete cds
1556	11490	21351		1.38	2.3E-01 A245480.1	NT	Brassica rapa ssp gene for S-locus glycoprotein, cultivar T2
1614	11518	21378		2.75	2.3E-01 Y10887.2	NT	Mus musculus cdh5 gene, exon 1, partial
1999	11892			1.3	2.3E-01 A/235353.1	NT	Homo sapiens partial intron 3 of the wild type AF-4/FFEL gene
2396	12274	22169		1.56	2.3E-01 BE97718.1	EST_HUMAN	60117562F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:3531016 5'
2615	12483	22372		1.02	2.3E-01 M11319.1	NT	Human erythropoietin gene, complete cds
2794	11271	21127		0.88	2.3E-01 AB015033.1	NT	Marinimilabia agarivorans gyrB gene for DNA gyrase subunit B, partial cds, strainnIFO 14957
2934	12861	22661		1.29	2.3E-01 AA601379.1	EST_HUMAN	not6dd6_s1 NCI_CGAP_Phe1 Homo sapiens cDNA clone IMAGE:1100843 3' similar to contains Alu repetitive element/contains element THR repetitive element;
3045	12972			5.73	2.3E-01 R21732.1	EST_HUMAN	Y121607_s1 Soares placenta Nb21F Homo sapiens cDNA clone IMAGE:130357 3'
3324	13244	23051		1.09	2.3E-01 H69836.1	EST_HUMAN	Y97H10_r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:213283 5'
3766	13679	23461		1.11	2.3E-01 S82821.1	NT	GSTA5=glutathione S-transferase Yc2 subunit {5' region, intron 1} [rats, Morris hepatoma cell line, Genomic, 22/12 nt, segment 1 of 3]
3856	13767			3.72	2.3E-01 7662133	NT	Homo sapiens KIAA0450 gene product (KIAA0450), mRNA
4253	14152	23926		0.85	2.3E-01 R82252.1	EST_HUMAN	Y17H01_r1 Soares placenta Nb21F Homo sapiens cDNA clone IMAGE:149017 5'
4300	14198			3.35	2.3E-01 L78739.1	NT	Mus musculus renin (Ren-1c) gene, promoter region
4349	14245	24031		1.02	2.3E-01 D00899.1	NT	Synechocystis sp. PCC6303 complete genome, 1/27, 1-133859
4386	14282	24061		2.08	2.3E-01 AF092535.1	NT	Homo sapiens mitogen-activated protein kinase p38delta (PPKM13) mRNA, complete cds
4454	14348	24140		5.1	2.3E-01 5031984	NT	Homo sapiens nuclear transport factor 2 (placental protein 15) (PP15) mRNA
4956	14668	24455		0.82	2.3E-01 J03280.1	NT	Human phenylethanolamine N-methyltransferase gene, complete cds
5002	14877	24641		0.95	2.3E-01 BF516135.1	EST_HUMAN	601896136F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4125368 5'
5101	14969	24745					Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (H-A-H) gene, RorC gene, and sodium phosphate transporter (NPT3) gene, complete cds
5146	15013	24783		26.95	2.3E-01 AE000240.1	NT	Escherichia coli K-12 MG1655 section 130 of 400 of the complete genome
5246	15169	24942		2.6	2.3E-01 AB040945.1	NT	Homo sapiens mRNA for KIAA1512 protein, partial cds
5332	15252	25074		1.71	2.3E-01 BF058381.1	EST_HUMAN	7k30b6_s1 NCI_CGAP_Ov8 Homo sapiens cDNA clone IMAGE:3476698 3' similar to SW_GAG_SMSAV P03330 GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10] ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5395	15314	25361	4.83	2.3E-01	X96587.1	NT	C.familiaris rom1 gene
5618	15533	25617	1.87	2.3E-01	AI708840.1	EST_HUMAN	as27e12x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:231846 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
5618	15533	25618	1.87	2.3E-01	AI708840.1	EST_HUMAN	as27e12x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:231846 3' similar to gb:X13238 CYTOCHROME C OXIDASE POLYPEPTIDE VIC PRECURSOR (HUMAN);
6111	16005	26142	3.93	2.3E-01	AI718148.1	EST_HUMAN	as42f12x1 Barstead aorta HPLRB6 Homo sapiens cDNA clone IMAGE:2319887 3' similar to contains Aliu repetitive element;
6384	16246	26408	2.62	2.3E-01	AF175389.1	NT	Glycine max resistance protein LM17 precursor RNA, partial cds
6487	16345		3.19	2.3E-01	6754779	NT	Mus musculus myosin XV (Myo15), mRNA
6491	16349	26519	1.59	2.3E-01	BE880707.1	EST_HUMAN	601511573F1NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912859 5'
6560	16418		2.9	2.3E-01	NR0983.1	EST_HUMAN	zaf1e08.11 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone MAGE:292358 5'
6664	16544	26741	2.28	2.3E-01	MG6931.1	NT	Oxytricha nova macronuclear telomere-binding protein alpha subunit (tet(alpha alanine version) gene, complete cds
7657	17507	27732	1.37	2.3E-01	X52124.1	NT	Haemophilus influenzae genes for HinclI restriction-modification system (HincII methyltransferase (EC 2.1.1.72) and HinclI endonuclease (EC 3.1.21.4))
7712	17562	27787	2.54	2.3E-01	BE173050.1	EST_HUMAN	MR0-HT0556-240400-014-g11 HT0559 Homo sapiens cDNA
7740	17590	27811	2.26	2.3E-01	AI1293261.1	NT	Rhizobium leguminosarum partial genomic DNA for exopolysaccharide biosynthesis genes
7974	17824		4.95	2.3E-01	BF133577.1	EST_HUMAN	60164675R2 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102092 3'
8525	18397	28663	2.84	2.3E-01	A1250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
8525	18397	28664	2.84	2.3E-01	A1250189.1	NT	Mus musculus partial mRNA for muscle protein 534 (mg534 gene)
8658	18547	28830	2.39	2.3E-01	AE02167.2	NT	Chlamydophila pneumoniae Af39, section 4 of 94 of the complete genome
9144	18898		2.53	2.3E-01	U45426.1	NT	Borrelia burgdorferi 2.9.6 locus, ORFA-D genes, complete cds and REP+ gene, partial cds
9232	18951		20.46	2.3E-01	T27231.1	EST_HUMAN	HCOEST44 HT29M6 Homo sapiens cDNA clone HCoE44 5'
9258	19477		1.65	2.3E-01	AA089819.1	EST_HUMAN	chn1424.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'
9266	18970		2.07	2.3E-01	AW863940.1	EST_HUMAN	PM4-SN0012-030400-001-b06 SN0012 Homo sapiens cDNA
							xi21d07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813773 3' similar to TR-Q9Z175
9324	19665		2.05	2.3E-01	AW303623.1	EST_HUMAN	Q9Z175 LYSYL OXIDASE-RELATED PROTEIN 2; contains PTR5.b2 TAR1 repetitive element;
9358	19708	24905	4.88	2.3E-01	BE882464.1	EST_HUMAN	601507202F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3908689 5'
9407	19060		1.93	2.3E-01	BF663319.1	EST_HUMAN	602144459F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297719 5'
9456	19088		2.09	2.3E-01	AJ006519.1	NT	Rattus norvegicus mRNA for acid gated ion channel
9549	19088		4.54	2.3E-01	AJ006519.1	NT	nac39h12.x1 Lipsk1 sciatic_nerve Homo sapiens cDNA clone IMAGE:3395950 3' similar to contains element
9793	19310		2.67	2.3E-01	BF475611.1	EST_HUMAN	MER38 repetitive element;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
84	10068	19885	0.96	2.2E-01	A1052190.1	EST_HUMAN	ozt4at0x1 Soares_Fetal_liver_spleen_INF1S_S1 Homo sapiens cDNA clone IMAGE:1675290 3' similar to TR:Q13040 Q13040 ATP-BINDING CASSETTE PROTEIN ;
1545	11450	21311	3.13	2.2E-01	AF187850.1	NT	Homo sapiens PPAR delta gene, promoter region
1972	11895	-	0.91	2.2E-01	AF171901.1	NT	Trimeresurus malabaricus cytb gene, partial cds; mitochondrial gene for mitochondrial product
2042	11933	21829	2.78	2.2E-01	M34640.1	NT	Fresh-water sponge Emphi alpha collagen (COLF1) gene
2354	12234	22131	6.24	2.2E-01	BF677538.1	EST_HUMAN	602085608F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4249969 5'
2543	12417	22307	2.41	2.2E-01	BE618288.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3886190 5'
2543	12417	22308	2.41	2.2E-01	BE618288.1	EST_HUMAN	601462629F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3886190 5'
2853	12781	22570	4.04	2.2E-01	BE15625.1	EST_HUMAN	PM2-HT0353-281299-003-af12 HT0353 Homo sapiens cDNA
2853	12781	22571	4.04	2.2E-01	BE15625.1	EST_HUMAN	PM2-HT0353-281299-003-af12 HT0353 Homo sapiens cDNA
2890	12817		1.59	2.2E-01	AF020503.1	NT	Homo sapiens FRA3B common fragile region, diadenosine triphosphate hydrolase (FHT) gene, exon 5
3346	13266		2.67	2.2E-01	AL161582.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 62
3743	13655		1.05	2.2E-01	AF155728.1	NT	Xiphophorus maculatus truncated Rex1 retrotransposon reverse transcriptase (RT) pseudogene
4007	13913	23683	0.81	2.2E-01	AF213389.1	NT	Mus musculus ATP-binding cassette protein (Abcb8) mRNA, partial cds
4118	14018		1.19	2.2E-01	AF119102.1	NT	Drosophila melanogaster UNC-119 (unc-119) gene, complete cds
4125	14025	23800	5.07	2.2E-01	AF155142.1	NT	Mus musculus mixed lineage kinase 3 (Mll3) and two pore domain K+ channel subunit (Kcnh6) genes, complete cds
4166	14066	23840	1.97	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4166	14066	23841	1.97	2.2E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
4258	14157	23933	1.16	2.2E-01	U01307.1	NT	Human sRNA (BC200 beta) pseudogene
4258	14157	23934	1.16	2.2E-01	U01307.1	NT	Human sRNA (BC200 beta) pseudogene
4399	14294	24078	1.09	2.2E-01	Z54148.1	NT	B. abortus bp26 gene
4719	14605		1.22	2.2E-01	D50604.1	NT	Human beta-cytoplasmic actin (ACTBP9) pseudogene
4724	14610	24396	2.47	2.2E-01	AA211216.1	EST_HUMAN	zq87c051r1 Stratagene h1NT neuron (f#937233) Homo sapiens cDNA clone IMAGE:648968 5'
4891	14771	24549	1.19	2.2E-01	M86524.1	NT	Human dystrophin gene
4975	14850		1.2	2.2E-01	L13288.1	NT	Mus musculus vinculin gene, exon 3
5513	15431	25495	1.71	2.2E-01	5833002	NT	Homo sapiens diaphanous (Drosophila, homolog) 2 (DIAPH2), transcript variant 156, mRNA
5518	15436		3.99	2.2E-01	D64000.1	NT	Synechocystis sp. PCC6803 complete genome, 19/27, 2392729-2538999
6189	16074	26223	10.59	2.2E-01	AV756288.1	EST_HUMAN	AV7562238 BM Homo sapiens cDNA clone BMFAHC06 5'
6319	16182	26342	2.01	2.2E-01	M24136.1	NT	Human glycoprotein B gene, exon 4
6319	16182	26343	2.01	2.2E-01	M24136.1	NT	Human glycoprotein B gene, exon 4
6676	16556		2.19	2.2E-01	AF155143.1	NT	Mus musculus nm23-M1 gene, promoter region
7157	17034	27227	4.27	2.2E-01	AE001713.1	NT	Thermotoga maritima section 25 of 136 of the complete genome

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLASTE Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7217	17094			2.29	2.2E-01 AW855039.1	EST_HUMAN	PM3-CT0263-241289-009-b07 CT0263 Homo sapiens cDNA
7270	17147	27341		1.66	2.2E-01 8398247 NT		Mus musculus deformed epidermal autoregulatory factor 1 (Drosophila) (Dear1), mRNA
7304	17180	27382		1.39	2.2E-01 BF376354.1	EST_HUMAN	MR1-TN045-110900-006-c02 TN0045 Homo sapiens cDNA
7353	17221	27421		1.4	2.2E-01 W02988.1	EST_HUMAN	zad0f08_r1 Scarce melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:291591 5'
7366	17344	27550		13.13	2.2E-01 P48634	SWISSPROT	LARGE PROLINE-RICH PROTEIN BA12 (HLA-B-ASSOCIATED TRANSCRIPT 2)
7397	17315	27522		3.98	2.2E-01 M89643.1	NT	Brachydanois ferio epineymin beta and gamma chains (Epd) gene, complete cds
7648	17498	27720		3.57	2.2E-01 AF197941.1	NT	Funaria hygrometrica chloroplast-localized small heat shock protein (CPshSP21) mRNA, complete cds; nuclear gene for chloroplast product
7719	17569	27794		2.2	2.2E-01 BF206507.1	EST_HUMAN	601869724F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4100189 5'
8723	18540	28824		4.94	2.2E-01 X01918.1	NT	Drosophila 68C glue gene cluster
8756	17905	28149		2.91	2.2E-01 7706215 NT		Homo sapiens H-2K binding factor-2 (LOC51580), mRNA
9077	18854			2.2	2.2E-01 BE870959.1	EST_HUMAN	601446557F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3850670 5'
9183	19720			3.72	2.2E-01 U82671.2	NT	Homo sapiens chromosome Xq28 melanoma antigen family A2a (MAGEA2A), melanoma antigen family A12 (MAGEA12), melanoma antigen family A2b (MAGEA2B), melanoma antigen family A3 (MAGEA3), cathepsin (CALT), NAD(P)H dehydrogenase-like protein (NSDH-L), and Li>
9269	18973			2.34	2.2E-01 AF188643.1	NT	Vitis vinifera cultivar Pinot Noir plasma membrane aquaporin (PIP1a) mRNA, complete cds
9379	15093	24887		2.56	2.2E-01 AW361098.1	EST_HUMAN	RC1-CT0249-141199-021-g04 CT0249 Homo sapiens cDNA
9875	19713			3.75	2.2E-01 AV694801.1	EST_HUMAN	AV694801 GKC Homo sapiens cDNA clone GKCAHB02 5'
9855	10879	20727		1.74	2.1E-01 AA569289.1	EST_HUMAN	nm31e11_s1_NCI_CGAP_Lip2 Homo sapiens cDNA clone IMAGE:1081804
9553	10881	20729		0.9	2.1E-01 AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
1103	11023			2.16	2.1E-01 AE002314.2	NT	Chlamydia muridarum, section 45 of the complete genome
1180	11091	20936		1.24	2.1E-01 6754289 NT		Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
1180	11091	20937		1.24	2.1E-01 6754299 NT		Mus musculus interferon (alpha and beta) receptor 2 (Ifnar2), mRNA
							ok73ed2_s1_NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1519610 3' similar to gbk02765
1871	11767	21642		1.84	2.1E-01 AA806824.1	EST_HUMAN	COMPLEMENT C3 PRECURSOR (HUMAN);
2111	12000	21899		3.08	2.1E-01 BF95073.1	EST_HUMAN	602083129F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247503 5'
2894	12821	22613		1.65	2.1E-01 6912445 NT		Homo sapiens potassium voltage-gated channel, subfamily H (eag-related), member 4 (KCNH4), mRNA
3736	13648			5.05	2.1E-01 9838361 NT		Beta vulgaris mitochondrion, complete genome
3967	13874	23651		1.01	2.1E-01 P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
3967	13874	23652		1.01	2.1E-01 P11675	SWISSPROT	IMMEDIATE-EARLY PROTEIN IE180
4279	14178			1.28	2.1E-01 AB033041.1	NT	Homo sapiens mRNA for KIAA1245 protein, partial cds
4474	14398	24157		1.21	2.1E-01 AB010273.1	NT	Homo sapiens pshsp47 gene, complete cds
4786	14651	24439		1.26	2.1E-01 AJ009194.1	NT	Homo sapiens hox11 proto-oncogene, exons 1 to 3 and hug-1 gene

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
5134	15001	24772	0.99	2.1E-01	N98261.1	NT	Saccharomyces cerevisiae tau138 (TFC3) gene, complete cds	
5243	15167	24938	5.99	2.1E-01	BF672095.1	EST_HUMAN	6021520-01/F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4293001 5	
6123	15970	26106	1.86	2.1E-01	U04642.1	NT	Human olfactory receptor (OR17-2) gene, partial cds	
6385	16247			1.97	2.1E-01	AE000972.1	Archaeoglobus fulgidus section 135 of 172 of the complete genome	
6335	16393	26572	1.74	2.1E-01	AF000949.1	NT	Canis familiaris keratin (KRT9) gene, complete cds	
6559	16417	26596	1.35	2.1E-01	AF068687.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds	
6559	16417	26597	1.35	2.1E-01	AF068687.1	NT	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds	
6705	16585		1.21	2.1E-01	7305050	NT	Mus musculus erythrocyte protein band 4.1-like 3 (Epb4.1B3), mRNA	
							Haemophilus influenzae hmcD, putative haemocin processing protein (hmcC), putative ABC transporter (hmcB), putative haemocin structural protein (hmcA), and haemocin immunity protein (hmcI) genes, complete cds	
6951	16829	27022	4.78	2.1E-01	U68399.1	NT	S.cerevisiae chromosome II reading frame ORF YBL025w	
7224	17101	27289	5.88	2.1E-01	Z35786.1	NT	A.thaliana mRNA for ARanBP1b protein	
7479	17349	27553	2.36	2.1E-01	X97378.1	NT	Homo sapiens p53R2 gene for ribonucleotide reductase, exon 6	
7547	17398	27611	1.19	2.1E-01	AB036529.1	NT	Beta vulgaris mRNA for elongation factor 1-beta	
7917	17767	28006	2.49	2.1E-01	Z97067.1	NT	DIACYL GLYCEROL KINASE, DELTA (DIGLYCERIDE KINASE) (DGK-DELTA) (DAG KINASE DELTA)	
7929	17779	28018	1.49	2.1E-01	P52824	SWISSPROT	(80 KD DIACYL GLYCEROL KINASE)	
8849	18661		2.31	2.1E-01	11036617	NT	Homo sapiens pancreatic polypeptide 2 (PPY2), mRNA	
8862	18674	28964	2.15	2.1E-01	BE180422.1	EST_HUMAN	RC3-HT0622-040500-013-b11 HT0622 Homo sapiens cDNA	
9522	19132			1.6	2.1E-01	AF2217490.1	NT	Homo sapiens fragile 16D oxidoreductase (FOR) gene, exons 8, 9, and partial cds
9730	19634			1.4	2.1E-01	L32988.1	NT	Human granulin gene
9905	19382	25174	1.29	2.1E-01	BE672330.1	EST_HUMAN	7459e02x1 NCL CGAP_GCG Homo sapiens cDNA clone IMAGE:32228034 3'	
9979	19436		1.29	2.1E-01	5835904	NT	Salvinia alpinaus mitochondrial, complete genome	
193	10165	19983	1.72	2.0E-01	AB017437.1	NT	Gallus gallus mRNA for avena, complete cds	
523	10465		2.39	2.0E-01	7705601	NT	Homo sapiens CGI-18 protein (LOC51008), mRNA	
684	10617	20440	1.19	2.0E-01	M77055.1	NT	O.cuniculus germline IgH heavy chain V-H pseudogene, allele type VHα2	
793	10722	20563	1.81	2.0E-01	AF027865.1	NT	Mus musculus Major Histocompatibility Locus class II region	
985	10915	20759	1.03	2.0E-01	D80905.1	NT	Synecocystis sp. PCC6803 complete genome, 7/27, 781449-920915	
1109	11024	20866	2.57	2.0E-01	AL1632213.2	NT	Homo sapiens chromosome 21 segment HS21C013	
1234	11141	20983	1.42	2.0E-01	AJ152695.5	NT	Homo sapiens rac1 gene	
1286	11194	21047	1.29	2.0E-01	AW384997.1	EST_HUMAN	PM1-HT0422-29/299-002-006 HT0422 Homo sapiens cDNA	
1471	11376	21241	13.51	2.0E-01	4503408	NT	Homo sapiens dystrobevin, alpha (DTNA), mRNA	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
1534	11438	21295	2.51	2.0E-01	AB007974.1	NT	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0505
1538	11442	21300	1.59	2.0E-01	AF260700.1	NT	Homo sapiens sodium/iodide symporter mRNA, partial cds
1688	11590		1.82	2.0E-01	AF11170.3	NT	Homo sapiens 14q32.3 Jagged2 gene, complete cds; and unknown gene
1723	11624		1.64	2.0E-01	U67525.1	NT	Methanococcus jannaschii section 67 of 150 of the complete genome
1847	11743	21618	1.33	2.0E-01	BE871330.1	EST_HUMAN	601449411F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE3853330 5'
1847	11743	21619	1.33	2.0E-01	BE871330.1	EST_HUMAN	601449411F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE3853330 5'
2239	12181		1.67	2.0E-01	X82877.1	NT	H_sapiens Na+-D-glucose cotransport/regulator gene
2861	12789		0.95	2.0E-01	AF074890.1	NT	Homo sapiens full length insert cDNA YH85A11
3442	13359	23168	0.8	2.0E-01	P46807	SWISSPROT	HOMEBOX PROTEIN GLABRA2 (HOMEBOX-LEUCINE ZIPPER PROTEIN ATHB-10) (HD-ZIP PROTEIN ATHB-10)
3520	13436		0.89	2.0E-01	AW238005.1	EST_HUMAN	XP156022X1 NC1_CGAP_HN9 Homo sapiens cDNA clone IMAGE2740395 3' similar to contains element MER21 repetitive element;
3646	13560	23348	0.81	2.0E-01	P34641	SWISSPROT	CED-11 PROTEIN
3945	13853	23628	0.8	2.0E-01	X83997.1	NT	C.parasitica eapC gene
4464	14358		8.47	2.0E-01	BE826165.1	EST_HUMAN	QV4-EN0032-190500-223-e03 EN0032 Homo sapiens cDNA
4859	14739	24519	1.07	2.0E-01	AF147083.1	NT	Homo sapiens gamma-glutamyl hydrolase gene, exons 8 and 9 and complete cds
4972	14847	24616	6.07	2.0E-01	892200801NT	NT	Homo sapiens hypothetical protein ASH1 (ASH1), mRNA
5041	14913	24687	1.1	2.0E-01	Y19216.1	NT	Homo sapiens putative PsiHbD pseudogene for hair keratin, exons 1 to 9
5342	15263	25059	2.55	2.0E-01	X56600.1	NT	Rat SOD-2 gene for manganese-containing superoxide dismutase
5510	15428	25491	2.13	2.0E-01	114325401NT	NT	Homo sapiens dual oxidase-like domains 2 (DUOX2), mRNA
5694	15603	25705	5.29	2.0E-01	U15300.1	NT	Saccharomyces cerevisiae Hal5p (HAL5) mRNA, complete cds
5874	15780	25900	4.31	2.0E-01	X61033.1	NT	M.auratus mu class glutathione transferase gene
5934	15839	25962	3.54	2.0E-01	AW300865.1	EST_HUMAN	PM1-CT0247-14/099-001-g016 CT0247 Homo sapiens cDNA
6637	16517		6.95	2.0E-01	AF028026.1	NT	Andes virus strain O123/33 glycoprotein G1 and G2 precursor, gene, partial cds
6772	16651	26839	4.18	2.0E-01	X91151.1	NT	M.musculus scp2 gene exon 14
7511	17299		4.39	2.0E-01	AE001278.1	NT	Chlamydia trachomatis section 5 of 87 of the complete genome
7692	17542		2.07	2.0E-01	AF143692.1	NT	Homo sapiens filamin 2 (FLN2) mRNA, complete cds
7774	17624	27857	1.95	2.0E-01	AF083697.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
7774	17624	27858	1.95	2.0E-01	AF083697.1	NT	Arabidopsis thaliana root gravitropism control protein (PIN2) gene, complete cds
8214	18098	28350	2.7	2.0E-01	D89088.1	NT	Salvelinus pluvialis mRNA for transferrin, complete cds
8214	18098	28351	2.7	2.0E-01	D89088.1	NT	Salvelinus pluvialis mRNA for transferrin, complete cds
9503	19118		1.37	2.0E-01	AF206697.2	NT	Pimephales promelas liver glucose-6-photase-1-dihydrogenase mRNA, partial cds
9747	19308	25202	3.22	2.0E-01	AI023592.1	EST_HUMAN	ov80af10_s1 Soares_tstis_NH Homo sapiens cDNA clone IMAGE1643610 3'
9769	19288		6.61	2.0E-01	AF078164.2	NT	Homo sapiens Ku70-binding protein (KUB3) mRNA, partial cds

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9897	19374	25193		1.5	2.0E-01	11528495	NT
105	10086			10.35	1.9E-01	7549743	NT
349	10308	20126		6	1.9E-01	AF004353.1	NT
640	10577	20392		1.31	1.9E-01	U32581.2	NT
640	10577	20393		1.31	1.9E-01	U32581.2	NT
647	10584	20400		5.37	1.9E-01	BE070801.1	EST_HUMAN
648	10584	20400		7.32	1.9E-01	BE070801.1	EST_HUMAN
970	10893			1.61	1.9E-01	7305180	NT
1088	11004	20846		9.3	1.9E-01	AA3568813.1	EST_HUMAN
1348	11254	21110		2.3	1.9E-01	AF061282.1	NT
1416	11322			3.91	1.9E-01	AF134623.1	NT
2330	12211	22109		3.31	1.9E-01	8922553	NT
2892	12819	22611		3.91	1.9E-01	U66068.1	NT
2908	12834			5.55	1.9E-01	J00522.1	NT
3349	13269	23072		3.4	1.9E-01	D13197.1	NT
3434	13351	23156		4.63	1.9E-01	R16467.1	EST_HUMAN
3735	13647	23432		0.93	1.9E-01	AF264017.1	NT
3762	13675	23457		0.96	1.9E-01	P39768	SWISSPROT
3910	13820	23600		3.02	1.9E-01	AB006784.1	NT
3992	13899	23676		1.89	1.9E-01	AW754106.1	EST_HUMAN
4138	14038	23813		1.06	1.9E-01	BE834943.1	EST_HUMAN
4369	14265	24049		0.89	1.9E-01	AL161493.2	NT
4662	14548	24338		0.84	1.9E-01	Z93780.1	NT
4912	14791	24566		0.86	1.9E-01	AW49203.1	EST_HUMAN
4943	14821			1.04	1.9E-01	AF228642.1	NT
4962	14837	24605		1.11	1.9E-01	Q95239	SWISSPROT
5031	14903	24675		1.03	1.9E-01	AJ251176.1	NT
5113	14981	24755		0.99	1.9E-01	Z70296.1	NT
5123	14991			1.19	1.9E-01	AI631199.1	EST_HUMAN
5153	15020	24789		0.99	1.9E-01	6679085	NT
5441	15361			4.28	1.9E-01	AW130149.1	EST_HUMAN
5466	15386	25446		7.67	1.9E-01	AF127937.1	NT

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5588 15503		2.26	1.9E-01	AU133116.1	EST_HUMAN	AU133116 NT2RP4 Homo sapiens cDNA clone NT2RP400 3' similar to contains MER13	
6162 15119	24863	1.7	1.9E-01	R43212.1	EST_HUMAN	Yg09at2.1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:31663 3' similar to contains MER13	
6423 16284	26446	1.43	1.9E-01	U80922.1	NT	Arabidopsis thaliana serine/threonine protein phosphatase type one (TOPP8) gene, complete cds	
6449 16310	26476	3.06	1.9E-01	AF072724.1	NT	Zea mays starch branching enzyme (sbe1) gene, complete cds	
6658 16538	26735	1.62	1.9E-01	AL161557.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 57	
7041 16918	27109	12.89	1.9E-01	AB033024.1	NT	Homo sapiens mRNA for KIAA1198 protein, partial cds	
8038 17930	28176	2.16	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15	
8038 17930	28177	2.16	1.9E-01	AL161503.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 15	
8137 18025	28271	1.75	1.9E-01	AF228391.1	NT	Homo sapiens calcium channel alpha1E subunit (CACNA1E) gene, exons 7-49, and partial cds, alternatively spliced	
8981 18768	29060	2.61	1.9E-01	AJ248213.1	NT	Homo sapiens partial 5-HT4 receptor gene, exons 2 to 5	
9546 19146		1.67	1.9E-01	AF055900.1	NT	Drosophila melanogaster clathrin light chain mRNA, complete cds	
9880 19546		1.26	1.9E-01	AF001168.1	NT	Arabidopsis thaliana receptor-like kinase LECRK1 (LECRK1) gene, complete cds	
29 10016	19811	2.26	1.8E-01	U73200.1	NT	Mus musculus p116Rip mRNA, complete cds	
260 12663	20041	1.22	1.8E-01	AB022090.1	NT	Mus musculus Cct6 gene for chaperonin containing TCP-1 gamma subunit, partial cds	
366 10322	20145	2.41	1.8E-01	4502532	NT	Homo sapiens calcium channel, voltage-dependent, beta 2 subunit (CACNB2) mRNA, and translated products	
729 10661	20493	2.15	1.8E-01	AB021490.2	NT	Oryzias latipes gene for membrane guanylyl cyclase OlgC1, complete cds	
966 10889	20735	0.85	1.8E-01	AJ912212.1	EST_HUMAN	wd71f02_x1 NCI CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2337051 3	
1075 10990	20832	1.21	1.8E-01	AF000580.1	NT	Dicyostelium discoideum plasmid Ddp5, complete genome	
1267 11174	21024	5.28	1.8E-01	AL117189.1	NT	Yersinia pestis plasmid pCD1	
1487 11392	21252	1.29	1.8E-01	6753947	NT	Mus musculus guanylyl nucleotide binding protein 1 (Gbp1), mRNA	
1487 11392	21253	1.29	1.8E-01	6753947	NT	Mus musculus guanylyl nucleotide binding protein 1 (Gbp1), mRNA	
1803 11700		0.92	1.8E-01	4505036	NT	Homo sapiens latent transforming growth factor beta binding protein 4 (LTBP4) mRNA	
1823 11720		1.93	1.8E-01	AJ733708.1	EST_HUMAN	q922d10_x5 NCI CGAP_Kid8 Homo sapiens cDNA clone IMAGE:1761811 3' similar to TR.O76336 O75336 GAMMA BUTYROBETAIN HYDROXYLASE ;	
1873 11769	21644	1.6	1.8E-01	AB051897.1	NT	Mus musculus Scy46, Scy49, Scy16-ps, Scy16 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scy416 pseudogene, small inducible cytokine A5 precursor, complete cds	
2660 12527		2.99	1.8E-01	AW935728.1	EST_HUMAN	QV3-DT0018-081299-036-904 DT0018 Homo sapiens cDNA	
2868 12796		1.61	1.8E-01	AF184589.1	NT	Jonesidium aculeatum LFAY protein (LFAY2) gene, partial cds	
2873 12800	22595	1.09	1.8E-01	AW182300.1	EST_HUMAN	XJ41a33_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2659756 3	
3085 13012	22803	1.28	1.8E-01	AW985178.1	EST_HUMAN	QV0-BN0041-070300-147-004 BN0041 Homo sapiens cDNA	

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3570	13484	23275	1.07	1.8E-01	H03369.1	EST_HUMAN	Y45e01.1\$1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:1517043' similar to contains Alu repetitive element,
3570	13484	23276	1.07	1.8E-01	H03369.1	EST_HUMAN	Y45e01.1\$1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:1517043' similar to contains Alu repetitive element,
4154	14054	23828	0.8	1.8E-01	AJ221735.1	NT	Homo sapiens Xq pseudobautosomal region, segment 1/2
4238	14137		1.13	1.8E-01	D37954.1	NT	Bovine NB25 mRNA for MHC class II (BOLA-DQB), complete cds
4456	14350	24141	5.12	1.8E-01	AL161556.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 56
4663	14549	24639	2.36	1.8E-01	AB051897.1	NT	Mus musculus Scyaa, Scyab, Scya8, Scya16-ps, Scya5 genes for small inducible cytokine A6 precursor, small inducible cytokine A9 precursor, Scyai6 pseudogene, small inducible cytokine A5 precursor, complete cds
4770	14586	24677	0.93	1.8E-01	X92179.1	NT	S.tuberousum mRNA for alcohol dehydrogenase
4977	14852	24618	1.77	1.8E-01	AW314270.1	EST_HUMAN	MR3-ST0203-15/1299-112-906 ST0203 Homo sapiens cDNA
5027	14900	24670	4.17	1.8E-01	AF181258.1	NT	Mesocricetus auratus Na-taurocholate cotransporting polypeptide mRNA, partial cds
5053	14925	24697	1.28	1.8E-01	AI439881.1	EST_HUMAN	Y576e04.x1 NC1 CGAP Lym12 Homo sapiens cDNA clone IMAGE:2134590 3'
5117	14985			1.03	AJ000742.1	NT	Homo Sapiens hist11 gene, 5' UTR
5549	15465	25635	1.41	1.8E-01	AL161594.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 90
5922	15827	25952	1.29	1.8E-01	Q9QY14	SWISSPROT	FORKHEAD BOX PROTEIN E3
5948	15853		2.5	1.8E-01	N94853.1	EST_HUMAN	Yy62h02.1\$1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:278163 5'
6179	16065	26214	1.38	1.8E-01	AB018561.1	NT	Citrus lanatus mRNA for wsls, complete cds
6179	16065	26215	1.38	1.8E-01	AB018561.1	NT	Citrus lanatus mRNA for wsls, complete cds
7382	17251	27456	1.72	1.8E-01	M73258.1	NT	Human cellular DNA/Human papillomavirus proviral DNA
7396	17314	27521	1.22	1.8E-01	96262522	NT	Bacteriophage l1e, complete genome
7933	17783	28022	1.19	1.8E-01	X63440.1	NT	M.musculus mRNA for P19_protein tyrosine phosphatase
8033	17925	28172	3.19	1.8E-01	X77336.1	NT	A.thaliana mRNA for ribonucleotide reductase R2
8065	17956	28205	6.65	1.8E-01	U38906.1	NT	Bacteriophage r1t integrase, repressor protein (r1o), dUTPase, holin and lysin genes, complete cds
8118	18065	28214	2.9	1.8E-01	AB018561.1	NT	Citrus lanatus mRNA for wsls, complete cds
8118	18065	28215	2.9	1.8E-01	AB018561.1	NT	Citrus lanatus mRNA for wsls, complete cds
8119	18007	28264	3.88	1.8E-01	AF019107.1	NT	Dicyostelium discoideum unknown (DG1041) gene, complete cds
8381	18258	28507	2.64	1.8E-01	M59257.1	NT	Human carboembryonic antigen (CEA) gene, exon 4
8758	17907	28152	3.98	1.8E-01	X57033.1	NT	B.taurus mRNA for potassium channel
8876	18181	29073	2.83	1.8E-01	8394421	NT	Rattus norvegicus Trionitroxane receptor (Tbx2a2), mRNA
9169	18912	25344	1.65	1.8E-01	BF348623.1	EST_HUMAN	60201928F1 NCI_OGAP Bm67 Homo sapiens cDNA clone IMAGE:4155918 5'
9625	19200		2.05	1.8E-01	Q96682	SWISSPROT	DNA TERMINAL PROTEIN (BELLETT PROTEIN) (PTP PROTEIN)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor	
9798	19272	7.94	1.8E-01	R24494.1	EST_HUMAN	yr48h10.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:133027 5'		
9779	19294	1.63	1.8E-01	Y1114.1	NT	E_dispar mRNA for hexokinase (hxa1)		
5633	10503	1.8	1.7E-01	BE385164.1	EST_HUMAN	601274604F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3615768 5'		
788	10717	2.04	1.7E-01	X63330.1	NT	P_dumerilii histone gene cluster for core histones H2A, H2B, H3 and H4		
945	10870	1.89	1.7E-01	P35616	SWISSPROT	NEUROFILAMENT TRIPLET 1 PROTEIN (NEUROFILAMENT LIGHT POLYPEPTIDE) (NFE-L)		
1042	10960	1.6	1.7E-01	AF081810.1	NT	Lymantria dispar nucleopolyhedrovirus, complete genome		
1042	10960	1.6	1.7E-01	AF081810.1	NT	Lymantria dispar nucleopolyhedrovirus, complete genome		
1938	11533	3.8	1.7E-01	AF255051.1	NT	Homo sapiens BNIP3H (BNIP3H) gene, complete cds; nuclear gene for mitochondrial product		
2829	12758	22548	1.93	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL_VIBCO gene, partial cds	
2829	12758	22549	1.93	1.7E-01	AF000716.1	NT	Vibrio cholerae hypoxanthine phosphoribosyltransferase (hpt) gene, partial cds, hemagglutinin/protease regulatory protein (hapR) gene, complete cds, and YRAL_VIBCO gene, partial cds	
2896	12823	22616	1.74	1.7E-01	AA336909.1	EST_HUMAN	EST14651 Endometrial tumor Homo sapiens cDNA 5' end	
2967	12894	22693	1.35	1.7E-01	AJ238736.1	NT	Naja naja atra cik-1 gene, exons 1-3	
2967	12894	22694	1.35	1.7E-01	AJ238736.1	NT	Naja naja atra cik-1 gene, exons 1-3	
3067	12894	22785	1.89	1.7E-01	AF081514.1	NT	Taxus canadensis geranylgeranyl diphosphate synthase mRNA, complete cds	
3401	13318	23119	1.96	1.7E-01	AJ263505.1	NT	Anabaena sp. ORF4 (partial), ORF3, ORF2, ORF1, adpF gene, adpA gene, adpB gene, adpC gene, adpD gene, adpE gene and adpF gene	
3557	13471	23282	1	1.7E-01	AJ224877.1	NT	Homo sapiens nap1 gene, complete CDS	
3859	13770	23562	4.41	1.7E-01	AJ235377.1	NT	Homo sapiens derivative 11 breakpoint fragment: partial intron 10 of the ALL-1/MLL-HRX gene fused to intron 5 of the AF-4/FEFL gene	
4459	14353		1.88	1.7E-01	X5236.1	NT	Schistocerca gregaria alpha repetitive DNA	
4732	14617	24403	1.4	1.7E-01	AJ247635.1	EST_HUMAN	qf57e09 X1 Soares_fetal_liver_spleen_1NF1S_S1 Homo sapiens cDNA clone IMAGE:1848808 3' similar to qf57e09 X1 Soares_fetal_liver_spleen_1NF1S_S1 Homo sapiens cDNA clone IMAGE:1848808 3'	
4986	14861		1.16	1.7E-01	U28376.1	NT	contains ORF.b1 ORF repetitive element ;	
5067	14937		1.18	1.7E-01	AF072725.1	NT	Zea mays starch branching enzyme III (ae) gene, complete cds	
5321	15241	25046	1.76	1.7E-01	AA470686.1	EST_HUMAN	ne13a2.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);	
5321	15241	25047	1.76	1.7E-01	AA470686.1	EST_HUMAN	ne13a2.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:881066 3' similar to gb:M17886 60S ACIDIC RIBOSOMAL PROTEIN P1 (HUMAN);	
5820	15726	25839	12.31	1.7E-01	H72118.1	EST_HUMAN	ys02g06.s1 Soares fetal liver spleen 1NF1S Homo sapiens cDNA clone IMAGE:213658 3'	
6112	16006		2.15	1.7E-01	AF026552.3	NT	Mesociteetus auratus oriductin precursor (OVI) gene, complete cds	

Table 4

Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6320	16183	26344	7.96	1.7E-01	BE734179.1	EST_HUMAN	601568022F1 NIH_MGGC_21 Homo sapiens cDNA clone IMAGE:3843964 5'
6588	16468	266558	1.2	1.7E-01	AF000573.1	NT	Homo sapiens homogenilase 1 2-dicloxygenase gene, complete cds
6814	16693	26882	7.03	1.7E-01	7706426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
6814	16693	26883	7.03	1.7E-01	7706426	NT	Homo sapiens cleavage and polyadenylation specificity factor 3, 73kD subunit (CPSF3), mRNA
7066	16943	27135	2.46	1.7E-01	D00384.1	NT	Rat (ShIR strain) SK1 gene
7531	17382	27593	7.38	1.7E-01	AP001508.1	NT	Bacillus halodurans genomic DNA, section 2/14
7601	17452	27666	2.06	1.7E-01	U16288.1	NT	Human class IV alcohol dehydrogenase (ADH7) gene, exon 3
7875	17725		2.42	1.7E-01	AL103284.2	NT	Homo sapiens chromosome 21 segment HS21C034
7942	17792	28032	1.48	1.7E-01	11427203	NT	Homo sapiens solute carrier family 7 (cationic amino acid transporter, y ⁺ system), member 2 (SLC7A2), mRNA
7943	17793	28033	1.57	1.7E-01	AA627972.1	EST_HUMAN	ng60e07_s1 NCI_CGAP_C99 Homo sapiens cDNA clone IMAGE:1148292 3' similar to gb:L25081
8067	17958	28208	9.13	1.7E-01	BE309835.1	EST_HUMAN	TRANSFORMING PROTEIN RHOC (HUMAN); 601286547F1 NIH_MGGC_44 Homo sapiens cDNA clone IMAGE:3613258 5'
8182	18063	28317	2.47	1.7E-01	AA814617.1	EST_HUMAN	of48a03_s1 NCI_CGAP_CNS1 Homo sapiens cDNA clone IMAGE:126924 3'
8456	18329	28589	7.88	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
8456	18329	28590	7.88	1.7E-01	7106300	NT	Mus musculus adenomatosis polyposis coli binding protein Eb1 (Eb1), mRNA
8949	18757		1.92	1.7E-01	P15272	SWISSPROT	AMP NUCLEOSIDASE
9012	18811	29107	4.38	1.7E-01	11418157	NT	Homo sapiens calcium channel, voltage-dependent, alpha 1I subunit (CACNA1I), mRNA
9139	19666		1.5	1.7E-01	AL103278.2	NT	Homo sapiens chromosome 21 segment HS21C034
9420	19513		1.28	1.7E-01	AI824404.1	EST_HUMAN	txS9q5x1 NCI_CGAP_U11 Homo sapiens cDNA clone IMAGE:2274872 3' similar to gb:M73779 RETINOIC ACID RECEPTOR ALPHAI-1 (HUMAN);
9705	19253	26218	5.79	1.7E-01	U01317.1	NT	Human beta globin region on chromosome 11
120	10097	19917	1.88	1.6E-01	AF217532.1	NT	Human sapiens mevalonate kinase gene, exon 6 and 7
664	12641	20416	1.53	1.6E-01	R31497.1	EST_HUMAN	Yh75f12_r1 Soares placentae Nb214P Homo sapiens cDNA clone IMAGE:135599 5'
1505	11409	21268	4.05	1.6E-01	AF208117.1	NT	Homo sapiens homeobox protein OTX2 gene, complete cds
1882	11778	21653	2.4	1.6E-01	P22063	SWISSPROT	AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1)
1941	11836		1	1.6E-01	U10334.1	NT	Crassostrea gigas RNA polymerase II largest subunit mRNA, partial cds
2335	12719	22115	0.96	1.6E-01	X94332.1	NT	H. sapiens mRNA for novel T-cell activation protein
2443	12320	22218	2.19	1.6E-01	AB037729.1	NT	Homo sapiens mRNA for KIAA1308 protein, partial cds
2863	12791	22853	8.9	1.6E-01	AF156589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
2863	12791	22854	8.9	1.6E-01	AF156589.1	NT	Homo sapiens cytochrome P450 3A4 (CYP3A4) gene, promoter region
3581	13495	23285	1.31	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichocel AB13 gene
3581	13495	23286	1.31	1.6E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichocel AB13 gene
3919	13828		2.61	1.6E-01	AE004413.1	NT	Vibrio cholerae chromosome II, section 70 of the complete chromosome

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4234	14132	23908	7.92	1.6E-01	AF179680.1	NT	Homo sapiens apelin gene, complete cds
4353	14249		2.44	1.6E-01	AW068601.1	EST_HUMAN	EST38067 MAGE resequences, MAGU Homo sapiens cDNA
4361	14257		4.01	1.6E-01	6753319	NT	Mus musculus chaperonin subunit 3 (gamma) (Ccp3), mRNA
4781	14665	24451	0.86	1.6E-01	Z28330.1	NT	S.cerevisiae chromosome XI reading frame ORF YKR105c
4781	14665	24452	0.86	1.6E-01	Z28330.1	NT	S.cerevisiae chromosome XI reading frame ORF YKR105c
4865	14745	24624	1.14	1.6E-01	AA088343.1	EST_HUMAN	2184h09.s1 Stratagene colon (#37204) Homo sapiens cDNA clone IMAGE:511361 3' similar to TR: E221955
4869	14769	24546	1.92	1.6E-01	AJ006356.1	NT	Lyopersicon esculentum RsaI fragment 2, satellite region
4889	14769	24547	1.92	1.6E-01	AJ006356.1	NT	Lyopersicon esculentum RsaI fragment 2, satellite region
4958	14833	24601	1.09	1.6E-01	BE018707.1	EST_HUMAN	6683h08 y NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3049023 5' similar to gb:M61715
5390	15309	25162	3.12	1.6E-01	AW197496.1	EST_HUMAN	TRYPTOPHANYL-TRNA SYNTHETASE (HUMAN); gb:X69657 M.musculus (MOUSE);
5390	15309	25163	3.12	1.6E-01	AW197496.1	EST_HUMAN	xm43t01.x1 NCL_CGAP_GCG Homo sapiens cDNA clone IMAGE:2688969 3' similar to TR: O75984 O75984
5398	15317	25364	2.07	1.6E-01	AF034716.1	NT	Rattus norvegicus CCAAT/enhancer binding protein epsilon (cebp ϵ) gene, complete cds
5873	15779	25598	2.24	1.6E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
5873	15779	25599	2.24	1.6E-01	AL161588.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 84
6157	15115	24858	3.7	1.6E-01	AW291215.1	EST_HUMAN	UI-H-B12-agl-b-06-0-U1_S1 NCL_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:27244183
6571	16429	26612	1.84	1.6E-01	AW246359.1	EST_HUMAN	2822248.5prime NH_MGC_7 Homo sapiens cDNA clone IMAGE:2822248 5'
6592	16472	26662	1.42	1.6E-01	L49349.1	NT	Gorilla gorilla androgen receptor gene, partial exon
7187	17064	27254	1.89	1.6E-01	Z49801.1	NT	S.cerevisiae chromosome X reading frame ORF YIR001w
7564	17415		1.7	1.6E-01	BF375171.1	EST_HUMAN	RC3-ST0200-041199-011-h01 ST0200 Homo sapiens cDNA
7565	17416	27631	1.91	1.6E-01	Z49801.1	NT	S.cerevisiae chromosome X reading frame ORF YIR001w
8049	17940	28190	2.71	1.6E-01	AW850853.1	EST_HUMAN	113-CT0220-111199-028-G01 CT0220 Homo sapiens cDNA
8364	18241	28490	1.78	1.6E-01	O14647	SWISSPROT	CHROMODOMAIN+HELIcase-DNA-BINDING PROTEIN 2 (CHD-2)
8364	18241	28491	1.78	1.6E-01	O14647	SWISSPROT	CHROMODOMAIN+HELIcase-DNA-BINDING PROTEIN 2 (CHD-2)
8459	18332		7.6	1.6E-01	AF106064.1	NT	Plasmidium falciparum calcium-dependent protein kinase-3 (cdk3) gene, complete cds
8713	18530	28814	10.07	1.6E-01	6671552	NT	Mus musculus adaptor-related protein complex AP-1, beta 1 subunit (Apb1), mRNA
9001	18804	29097	2.69	1.6E-01	AW877127.1	EST_HUMAN	QV2PT010-160400-133-a08 PT0010 Homo sapiens cDNA
9025	19678		2.17	1.6E-01	6679466	NT	Mus musculus protein kinase, cGMP-dependent, type II (Pfk2), mRNA
9141	18896	28795	2.33	1.6E-01	AV719585.1	EST_HUMAN	AV719585 GLC Homo sapiens cDNA clone GLCEMF07 5'
9565	19493		6.33	1.6E-01	AB045310.1	NT	Cucumis sativus KS mRNA for ent-kaurene synthase, complete cds
9727	19265		2.84	1.6E-01	AK024496.1	NT	Homo sapiens mRNA for FLJ00104 protein, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	(Top) Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
9807	19819		2.47	1.6E-01	AF287344.1	NT	Fuchsia hybrid cultivar Chi 94/208 ribosomal protein S10 gene, partial cds; nuclear gene for mitochondrial product
9827	19828	25208	1.27	1.6E-01	9506522	NT	Rattus norvegicus chondroitin sulfate proteoglycan 5 (neuroglycan C) (Cspg5), mRNA
248	10214	20030	1.87	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
248	10214	20031	1.87	1.5E-01	BE710087.1	EST_HUMAN	IL3-HT0619-040700-197-E05 HT0619 Homo sapiens cDNA
572	12640		2.28	1.5E-01	AV711696.1	EST_HUMAN	AV711696 DCA Homo sapiens cDNA clone DCA-DH06 5'
766	10697	20534	1.4	1.5E-01	AL153284.2	NT	Homo sapiens chromosome 21 segment HS21C034
1076	10992	20834	0.88	1.5E-01	AJ009735.1	NT	Cyprinus carpio mRNA for EGGS22 myosin heavy chain, 3'UTR
1081	10997	20838	1.87	1.5E-01	AJ251885.1	NT	Homo sapiens partial SLC22A2 gene for organic cation transporter (OCT2), exon 1
1097	11013		1.82	1.5E-01	L36125.1	NT	Rattus norvegicus insulin-responsive glucose transporter (GLUT4) gene, 5' end
1198	11108	20953	1.36	1.5E-01	AW195516.1	EST_HUMAN	xn39d11.x1 NCL_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2686086 3'
1254	11161	21010	2.81	1.5E-01	D26535.1	NT	Human gene for dihydrofolate succinyltransferase, complete cds (exon 1-5)
1254	11161	21011	2.81	1.5E-01	D26535.1	NT	Human gene for dihydrofolate succinyltransferase, complete cds (exon 1-5)
1466	11371	21238	1.49	1.5E-01	AF117340.1	NT	Mus musculus MAP kinase kinase kinase 1 (Mekk1) mRNA, complete cds
1866	11762	21636	1.54	1.5E-01	AW444451.1	EST_HUMAN	U1-H-B13-akb-b-09-0-U.s1 NCL_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2733864 3'
2679	12544	22435	1.12	1.5E-01	BF695381.1	EST_HUMAN	602083269F1 NIH MGCG_81 Homo sapiens cDNA clone IMAGE:4247537 5'
2699	12927	22719	0.89	1.5E-01	M81441.1	NT	Bos taurus factor V variant 2 (factor V) mRNA, complete cds
3308	13229	23034	4.22	1.5E-01	AA935049.1	EST_HUMAN	oc68d05.s1 NCL_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1571337 3' similar to gb:NM11433
3322	13242	23048	0.87	1.5E-01	Z23104.1	NT	RETINOL-BINDING PROTEIN 1, CELLULAR (HUMAN); L. signals mRNA for G protein-coupled receptor
3322	13242	23049	0.87	1.5E-01	Z23104.1	NT	L. signals mRNA for G protein-coupled receptor
3380	13298	23097	0.96	1.5E-01	AW612237.1	EST_HUMAN	hh29f02.x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:29566539 3' similar to contains element MER16 repetitive element;
3696	13610	23394	1.34	1.5E-01	U09964.1	NT	Mus musculus glyceraldehyde 3-phosphate dehydrogenase (Gapd-S) gene, complete cds
3706	13619	23403	185.26	1.5E-01	7108358	NT	Homo sapiens pyruvate dehydrogenase kinase, isozyme 1 (PDK1), nuclear gene encoding mitochondrial protein, mRNA
3791	13703	23490	2.35	1.5E-01	AW665983.1	EST_HUMAN	hj0f06.x1 Scores_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2981411 3'
3806	13718	23506	0.8	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichocarpa AB13 gene
3806	13718	23507	0.8	1.5E-01	AJ003165.1	NT	Populus trichocarpa cv. Trichocarpa AB13 gene
3964	13871	23649	0.96	1.5E-01	AW366689.1	EST_HUMAN	RC2-HT0149-19n099-012-c09 HT0149 Homo sapiens cDNA
4006	13912	23687	0.97	1.5E-01	Z12028.1	NT	B.napus mitochondrial DNA for ORF158
4091	13991	23768	8.36	1.5E-01	AL153284.2	NT	Homo sapiens chromosome 21 segment HS21C084
4623	14511	24201	1.34	1.5E-01	BF687665.1	EST_HUMAN	602067192F1 NIH MGCG_57 Homo sapiens cDNA clone IMAGE:4066223 5'

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4645	12544	22435	2.18	1.5E-01	BF895381.1	EST_HUMAN	602083269F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4247537 5'
4680	14566	24361	1.08	1.5E-01	BE173796.1	EST_HUMAN	CM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
4680	14566	24362	1.08	1.5E-01	BE173796.1	EST_HUMAN	CM0-HT0565-280200-245-b10 HT0565 Homo sapiens cDNA
4929	14808	24576	1.3	1.5E-01	AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60
5072	14942	24716	0.84	1.5E-01	AF03105.1	NT	Arabidopsis thaliana AP2 domain containing protein RAP2.12 mRNA, partial cds
5216	15139	24833	2.02	1.5E-01	P07996	SWISSPROT	THROMBOSPONDIN 1 PRECURSOR
5266	15188		5.87	1.5E-01	P15196	SWISSPROT	SEX HORMONE-BINDING GLOBULIN PRECURSOR (SHBG) (SEX STEROID-BINDING PROTEIN) (SBP) (TESTIS-SPECIFIC ANDROGEN-BINDING PROTEIN) (ABP)
5400	15319	25367	4.06	1.5E-01	AW860754.1	EST_HUMAN	IL3-CT0219-160200-064-F10 CT0219 Homo sapiens cDNA
5424	15345	25398	6.77	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGF- α) mRNA, complete cds
5424	15345	25399	6.77	1.5E-01	U65016.1	NT	Mus musculus transforming growth factor alpha (TGF- α) mRNA, complete cds
5652	15564	25660	1.9	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dmt2), mRNA
5652	15564	25661	1.9	1.5E-01	6753659	NT	Mus musculus DNA methyltransferase 2 (Dmt2), mRNA
5684	15593	25694	1.87	1.5E-01	AJ276505.1	NT	Mus musculus genomic fragment, 279 Kb, chromosome 7
5760	15688	25774	2.44	1.5E-01	BE1727638.1	EST_HUMAN	601564322F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3833981 5'
5785	15691		1.68	1.5E-01	4506398	NT	Homo sapiens RAD54 (S.cerevisiae)like (RAD54L) mRNA
5828	15734	25845	1.78	1.5E-01	AF134907.1	NT	Influenza B virus (B/Nanchang/480/94) NB protein gene, complete cds; and neuramidase gene, partial cds
5917	19455	25948	1.96	1.5E-01	AED01039.1	NT	Archaeoglobus fulgidus section 68 of 172 of the complete genome
5935	15840	25963	5.13	1.5E-01	11417236	NT	Homo sapiens chromosome 5 open reading frame 3 (C5ORF3), mRNA
5942	15847	25971	1.81	1.5E-01	P48508	SWISSPROT	GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN)
5972	15876	26000	2.09	1.5E-01	Q28462	SWISSPROT	AMELOGENIN
6031	15935	26067	1.4	1.5E-01	P30143	SWISSPROT	HYPOTHETICAL 51.7 KD PROTEIN IN THRC-TAL B INTERGENIC REGION (ORF8)
6166	15123	24866	5.63	1.5E-01	AW970295.1	EST_HUMAN	EST382376 MAGE sequences, MAGK Homo sapiens cDNA
6284	16148		1.77	1.5E-01	AF210842.1	NT	Homo sapiens HARP (HARP) gene, exon 17 and complete cds
6374	16236	26396	1.88	1.5E-01	A1973157.1	EST_HUMAN	wr52c08.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2491310 3'
6481	16340	26507	1.68	1.5E-01	AW500611.1	EST_HUMAN	U1-HF-BN0-akk-d-05-0-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
6481	16340	26508	1.68	1.5E-01	AW500611.1	EST_HUMAN	U1-HF-BN0-akk-d-05-0-U1r1 NIH_MGC_50 Homo sapiens cDNA clone IMAGE:3077409 5'
6786	16655	26856	1.22	1.5E-01	AA970317.1	EST_HUMAN	INTERLEUKIN-2 RECEPTOR BETA CHAIN PRECURSOR (HUMAN); C16800 Clontech human acta polyA+ mRNA (66572) Homo sapiens cDNA clone GEN:5229H08 5'
6895	16774		11.77	1.5E-01	C16800.1	EST_HUMAN	Pangasiandon gigas growth hormone (GH) mRNA, complete cds
6912	16790	26983	1.88	1.5E-01	L27385.1	NT	Pangasiandon gigas growth hormone (GH) mRNA, complete cds
6996	16873	27064	1.44	1.5E-01	D84476.1	NT	Homo sapiens mRNA for ASK1, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7130	17007	27200	1.71	1.5E-01	4501972 NT		Homo sapiens adaptor-related protein complex 1, beta 1 subunit (ADTB1), mRNA
7265	17142	27335	2.48	1.5E-01	N74226.1	EST_HUMAN	za59e06.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:296866 3' similar to PIR:S44443 S44443 RAD23 protein homolog2 - human ;
7306	17182		2.98	1.5E-01	AV754819.1	EST_HUMAN	AV754819.TP Homo sapiens cDNA clone TPAAH12.5
7438	16451	26641	6.6	1.5E-01	U00455.1	NT	Acipenser transmontano vitellogenin mRNA, partial cds
7706	17556	27781	7.02	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
7706	17556	27782	7.02	1.5E-01	AF007570.1	NT	Aplysia californica carboxypeptidase D mRNA, complete cds
7860	17710	27955	2.86	1.5E-01	X88852.1	NT	P. leniusculus mRNA for Integrin beta subunit
7908	17758	27998	2.45	1.5E-01	AI814046.1	EST_HUMAN	wk53h12.x1 NCI CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
7908	17758	27999	2.45	1.5E-01	AI814046.1	EST_HUMAN	wk53h12.x1 NCI CGAP_P122 Homo sapiens cDNA clone IMAGE:2419175 3' similar to gb:M27508 BETA GALACTOSIDASE-RELATED PROTEIN PRECURSOR (HUMAN);
7939	17789	28031	1.54	1.5E-01	U40932.1	NT	Danio rerio transcription factor Pax6b (Pax9) mRNA, complete cds
8009	17859	28103	1.35	1.5E-01	AJ011964.1	NT	Claviceps purpurea ps1 gene
8009	17859	28104	1.35	1.5E-01	AJ011964.1	NT	Claviceps purpurea ps1 gene
8199	18084	28334	5.15	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8199	18084	28335	5.15	1.5E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080
8342	18219		1.74	1.5E-01	AB042975.1	NT	Sus scrofa CYP51 gene for lanosterol 14 alpha-demethylase, exon 1
8425	18299	28555	1.73	1.5E-01	AW841919.1	EST_HUMAN	IL5:CN0024-030300-025:D04 CN0024 Homo sapiens cDNA
8506	16236	26396	2.17	1.5E-01	AI973157.1	EST_HUMAN	wf52c08.x1 NCI CGAP_U11 Homo sapiens cDNA clone IMAGE:2491310 3'
9009	19547		20.02	1.5E-01	BF700582.1	EST_HUMAN	602128753F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285549 5'
9531	19565		4.14	1.5E-01	RS3077.1	EST_HUMAN	yp87e04.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:194430 5'
9621	19588		2.14	1.5E-01	AV741272.1	EST_HUMAN	AV741272 CB Homo sapiens cDNA clone CBDA0D04.5'
9726	19497	25133	3.99	1.5E-01	AL130074.2	NT	Campylobacter jejuni NCTC11168 complete genome; segment 1/6
9892	19402	25119	3.01	1.5E-01	AJ275242.1	NT	Sus scrofa mRNA for sodium iodide symporter
9972	19432		1.58	1.5E-01	AF020346.1	NT	Rattus norvegicus pyridoxal kinase mRNA, complete cds
226	10280		1.96	1.4E-01	AF009663.1	NT	Homo sapiens T cell receptor beta locus, TCRBV1S242 region
892	10848		2.57	1.4E-01	DT8638.1	NT	Xenopus laevis mRNA for DNA (cytosine-5-) methyltransferase, complete cds
1238	11145		1.62	1.4E-01	T91894.1	EST_HUMAN	yd54c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:112032 3'
1714	11615		1.43	1.4E-01	6679980	NT	Mus musculus growth differentiation factor 5 (Gdf5), mRNA
1717	11618	21487	1.53	1.4E-01	AE001710.1	NT	Thermatoga maritima section 22 of 136 of the complete genome
1863	11159		0.94	1.4E-01	AW135741.1	EST_HUMAN	U1-H-B1-act-a-09-0-U1.s1 NCI CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2714009 3'
1942	11837		10.35	1.4E-01	AA720615.1	EST_HUMAN	mv72d07.s1 NCI CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1283821 31
2426	12503	22199	0.97	1.4E-01	P30706	SWISSPROT	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)

Table 4
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Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2762	12624	22517	3.07	1.4E-01	AI983496.1	EST_HUMAN	wm74d01_x1_NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2441665 3'
3823	13735	23524	1	1.4E-01	R59232.1	EST_HUMAN	yg97e03_r1 Soares_infant brain 1NIB Homo sapiens cDNA clone IMAGE:41467 5'
3823	13735	23525	1	1.4E-01	R59232.1	EST_HUMAN	yg97e03_r1 Soares_infant brain 1NIB Homo sapiens cDNA clone IMAGE:41467 5'
4083	13985	23162	8.38	1.4E-01	AI690934.1	EST_HUMAN	tk56c02_x1_NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4083	13985	231763	8.38	1.4E-01	AI690934.1	EST_HUMAN	tk56c02_x1_NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2273570 3'
4144	14044	23817	3.16	1.4E-01	AE001710.1	NT	Thermatoga maritima section 22 of 136 of the complete genome
4813	14210			0.8	1.4E-01	AA776287.1	EST_HUMAN
5032	14904			0.91	1.4E-01	AW386022.1	EST_HUMAN
5116	14984	24759	1	1.4E-01	AL163284.2	NT	Hom sapiens chromosome 21 segment HS21C034
5147	15014	24784	0.81	1.4E-01	AJ005180.1	NT	Lycopersicon esculentum genomic RAPD band 26
5248	15171	24844	4.5	1.4E-01	T90677.1	EST_HUMAN	ye15c11s1 Stratagene Lung #937210 Homo sapiens cDNA clone IMAGE:117812 3'
5267	15189	24863	4.29	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5267	16189	24864	4.29	1.4E-01	AB004556.1	NT	Candida tropicalis DNA for mitochondrial NADP-linked isocitrate dehydrogenase, complete cds
5805	15710	25623	2.72	1.4E-01	BE328891.1	EST_HUMAN	hr67c02_x1_NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3133558 3'
5903	15809	256334	5.64	1.4E-01	AU117147_HMBA1	EST_HUMAN	AU117147_HMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
5903	15809	256335	5.64	1.4E-01	AU117147_HMBA1	EST_HUMAN	AU117147_HMBA1 Homo sapiens cDNA clone HEMBA1000769 5'
5958	15863	256985	3.07	1.4E-01	AW082796.1	EST_HUMAN	xb71d12_x1_Soares_NFL_T_GBC_S11 Homo sapiens cDNA clone IMAGE:2581751 3'
5969	15874			1.56	1.4E-01	BE266536.1	EST_HUMAN
5982	15887	26009	1.89	1.4E-01	BF375533.1	EST_HUMAN	QY1-UM0036-080300-103-d09 UM0036 Homo sapiens cDNA
6371	16233			1.62	1.4E-01	AW015373.1	EST_HUMAN
6936	16814			1.33	1.4E-01	AV659047.1	EST_HUMAN
7467	17044	27236	4.48	1.4E-01	AA307073.1	EST_HUMAN	EST178192 Colon carcinoma (HCC) cell line Homo sapiens cDNA 5' end
7300	17176	27377	8.05	1.4E-01	BF310959.1	EST_HUMAN	6011895465F1_NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4124834 5'
7343	17211	27410	1.36	1.4E-01	W83411.1	EST_HUMAN	zg94a04_r1 Soares_fetal_heart_NbHH19N Homo sapiens cDNA clone IMAGE:357102 5' similar to contains element KER repetitive element;
7387	17256	27461	1.56	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
7387	17256	27462	1.56	1.4E-01	Y10196.1	NT	Homo sapiens PHEX gene
7436	16449	26639	2.03	1.4E-01	AF121361.1	NT	Drosophila melanogaster signal transducting adapter protein (DNZ1) genes, complete cds
8091	17982			2.02	1.4E-01	AA811480.1	EST_HUMAN
8216	18100	28552	3.28	1.4E-01	R53400.1	EST_HUMAN	Y70c05_r1 Soares_breast_2NbHBs1 Homo sapiens cDNA clone IMAGE:154088 5'
8613	18480	28751	1.89	1.4E-01	X66092.1	NT	C.perfringens ORF for putative membrane transport protein

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Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8764	17913	28158	2.23	1.4E-01	U28760.1	NT	Barrella burgdorferi glyceraldehyde-3-phosphate dehydrogenase (GAPDH), phosphoglycerate kinase (PGK), triosephosphate isomerase (TPI) genes, complete cds
8813	18626		3.02	1.4E-01	X52102.1	NT	M.musculus p16K gene for 16 kDa protein
9365	19517	25138	1.48	1.4E-01	AB000890.1	NT	Ephydium fluviatile mRNA for aldolase, partial cds
9413	19065	25277	2.32	1.4E-01	X74773.1	NT	P.sallina plastid gene secY
9427	19073		1.89	1.4E-01	11968117	NT	Rattus norvegicus desmin (Des), mRNA
9470	19734		1.82	1.4E-01	BE513802.1	EST_HUMAN	601315638F1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3634329 5'
9560	19156		3.01	1.4E-01	AF083221.1	NT	Fugu rubripes putative neurotransmitter receptors, YDR140w homolog, and glycaminide ribonucleotide transformylase (GART) genes, complete cds
9573	19163		2.29	1.4E-01	D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2868/767-3002965
9646	19754		3.28	1.4E-01	P10447	SWISSPROT	TYROSINE-PROTEIN KINASE TRANSFORMING PROTEIN AB
9762	19282		1.41	1.4E-01	BE782/38.1	EST_HUMAN	601465575F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3668795 5'
9831	19332		1.42	1.4E-01	11425031	NT	Homo sapiens ephrin-B3 (EFNB3), mRNA
9850	19566		3.41	1.4E-01	D82963.1	NT	Mus musculus mRNA for prolidase, complete cds
9826	19398		1.77	1.4E-01	AW377998.1	EST_HUMAN	MRO-HT0208-22/29/204-c08 HT0208 Homo sapiens cDNA
319	10281	20098	2.69	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
319	10281	20099	2.69	1.3E-01	4758467	NT	Homo sapiens G protein-coupled receptor 50 (GPR50) mRNA
518	10460	20271	1.86	1.3E-01	AB013139.1	NT	Homo sapiens gene for NBS1, complete cds
620	10557	20369	0.89	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NL/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NL/Girlington/93/UK
620	10557	20370	0.89	1.3E-01	AJ277606.1	NT	Human calicivirus HU/NL/Girlington/93/UK RNA for capsid protein (ORF2), strain HU/NL/Girlington/93/UK
826	10753	20603	1.09	1.3E-01	X53330.1	NT	P.dumerili histone gene cluster for core histones H2A, H2B, H3 and H4
876	10802	20652	1.83	1.3E-01	AF130518.1	NT	Rattus norvegicus A-kinase anchor protein mRNA, complete cds
1010	10928	20771	1.55	1.3E-01	AL117078.1	NT	Botrylloides cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1111	11026		2.23	1.3E-01	AL116265.1	NT	Botrylloides cinerea strain T4 cDNA library under conditions of nitrogen deprivation
1197	11107	20852	1.07	1.3E-01	AV712467	EST_HUMAN	AV712467 DCA_Homo sapiens cDNA clone DCAAFF05 5'
1426	11331		1.36	1.3E-01	AF146277.1	NT	Homo sapiens adapter protein CMS mRNA, complete cds
1916	11811	21689	2.56	1.3E-01	AL117078.1	NT	Botrylloides cinerea strain T4 cDNA library under conditions of nitrogen deprivation
2124	12012		1.29	1.3E-01	AJ243578.1	NT	Rhodopseudomonas acidophila puc55, pucA5, pucB6, pucA6, pucB7, pucA7, pucB8, pucA8 and pucC genes and ORF151
2245	12129		1.17	1.3E-01	AW312104.1	EST_HUMAN	RC4-ST0173-191099-392-412 ST0173 Homo sapiens cDNA
2329	12210		2.99	1.3E-01	AE001016.1	NT	Archaeoglobus fulgidus section 91 of 172 of the complete genome
2542	12416	22306	3.49	1.3E-01	M86918.1	NT	Carassius auratus keratin type I mRNA, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar BLAST E Value	(Top) Hit No.	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
3404	13321	23122	0.95	1.3E-01	M21_572.1	NT	Bovine branched chain alpha-keto acid dihydrodipoyl transacylase mRNA, complete cds	
3661	13575	23362	1.18	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt, position (1/17)	
3661	13575	23363	1.18	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt, position (1/17)	
3667	13581	23368	0.78	1.3E-01	AB032159.1	NT	Homo sapiens DD4 gene for dihydrodiol dehydrogenase 4 [AKR 1C4], exon 2	
3714	13575	23362	0.86	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt, position (1/17)	
3714	13575	23363	0.86	1.3E-01	AP000001.1	NT	Pyrococcus horikoshii OT3 genomic DNA, 1-287000 nt, position (1/17)	
3734	13646	23131	0.85	1.3E-01	6978840	NT	Rattus norvegicus Fibroningen, gamma polypeptide (Fgg), mRNA	
3906	13816		1.7	1.3E-01	AL161581.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 77	
4046	13948		1.15	1.3E-01	AF020713.1	NT	Bacteriophage SPBc2 complete genome	
4068	13968		3.44	1.3E-01	AW364341.1	EST_HUMAN	QV3-DT0018-081/299-036-a03 DT0018 Homo sapiens cDNA	
4075	13977	23756	1.89	1.3E-01	AF026805.1	NT	Schistosoma mansoni fructose bisphosphate adductase mRNA, complete cds	
4093	13993	23770	16.36	1.3E-01	AW273741.1	EST_HUMAN	x23f10.1x Soares, NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2813995 3'	
4192	14092	23870	0.85	1.3E-01	AV752279	EST_HUMAN	AV752279 NPD Homo sapiens cDNA clone NPDTZE02 5'	
4192	14092	23871	0.85	1.3E-01	AV752279	EST_HUMAN	AV752279 NPD Homo sapiens cDNA clone NPDTZE02 5'	
4218	14116		1.65	1.3E-01	AL163280.2	NT	Homo sapiens chromosome 21 segment HS21C080	
4433	14328	24116	2.16	1.3E-01	BE272339.1	EST_HUMAN	60112609651 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:2980063 5'	
4525	14418	24202	0.81	1.3E-01	BF679654.1	EST_HUMAN	60215130561 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295514 5'	
4771	15075		3.17	1.3E-01	BE884017.1	EST_HUMAN	60151034751 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3911987 5'	
4903	14783		0.86	1.3E-01	AU136619.1	EST_HUMAN	AU136619 PLACE1 Homo sapiens cDNA clone PLACE1004693 5'	
5074	14944	24718	1.21	1.3E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084	
5074	14944	24719	1.21	1.3E-01	AL163284.2	NT	Homo sapiens chromosome 21 segment HS21C084	
5173	15039	24805	0.9	1.3E-01	BF679819.1	EST_HUMAN	60215144101F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295305 5'	
5173	15039	24806	0.9	1.3E-01	BF679819.1	EST_HUMAN	60215144101F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4295305 5'	
5292	15213	25013	2.51	1.3E-01	AW304417.1	EST_HUMAN	QV0-UM0093-100400-189-a06 UM0093 Homo sapiens cDNA	
5428	15348		1.79	1.3E-01	AF056880.1	NT	Hepatitis C virus 68 Cl 10 genome polyprotein gene, partial cds	
5904	15810	25696	13.21	1.3E-01	AB031326.1	NT	Schizosaccharomyces pombe gene for Alp41, complete cds	
5956	15861	25693	2.04	1.3E-01	X8891.1	NT	Ciacchus nitron 4 of visual pigment gene (red allele)	
6305	16169		2	1.3E-01	HA8664.1	EST_HUMAN	yr33d02.1x Soares fetal liver spleen 1NFL S Homo sapiens cDNA clone IMAGE:207075 5'	
6649	16529	26723	1.34	1.3E-01	11423294	NT	Homo sapiens PRQ00611 protein (PRQ00611), mRNA	
6668	16548	26744	1.28	1.3E-01	BF690522.1	EST_HUMAN	60218701571 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'	
6658	16737		4.54	1.3E-01	Z74102.1	NT	S.cerevisiae chromosome IV reading frame ORF YD054c	
6686	16765		4.14	1.3E-01	8923919	NT	Homo sapiens core histone macroH2A.2 (MACROH2A.2), mRNA	
6960	16838	27031	1.27	1.3E-01	BF690522.1	EST_HUMAN	60218701571 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4299074 3'	
7452	17261	27467	4.45	1.3E-01	AF023129.1	NT	Oncotologus cuniculus H+K+-ATPase alpha 2c subunit mRNA, complete cds	

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8029	17921			2.88	1.3E-01	BF300999.1	EST_HUMAN
8444	18318	28577		1.83	1.3E-01	AF119117.1	NT
8576	18444			5.13	1.3E-01	6671745	NT
8873	18685	28976		3.72	1.3E-01	BE279449.1	EST_HUMAN
9261	18966	25320		1.97	1.3E-01	BE618846.1	EST_HUMAN
9299	19054			3.18	1.3E-01	AJ242790.1	NT
9757	19279			1.56	1.3E-01	AB026829.1	NT
9784	19297			1.32	1.3E-01	AW001114.1	EST_HUMAN
9945	19414			1.26	1.3E-01	BF577764.1	EST_HUMAN
378	10362	20185		7.21	1.2E-01	AI421744.1	EST_HUMAN
418	9985			1.55	1.2E-01	U68912.1	NT
535	10476			2.63	1.2E-01	AF039442.1	NT
1355	11261	21117		2.78	1.2E-01	AU149146.1	EST_HUMAN
1355	11261	21118		2.78	1.2E-01	AU149146.1	EST_HUMAN
1361	11267			3.94	1.2E-01	AV735249.1	EST_HUMAN
1490	11395			1.13	1.2E-01	AA897474.1	EST_HUMAN
1613	11517	21377		1.17	1.2E-01	Q14934	SWISSPROT
1631	11535	21396		2.62	1.2E-01	AI285402.1	EST_HUMAN
1730	11631			29.48	1.2E-01	X89211.1	NT
1877	11773			1.43	1.2E-01	AW449368.1	EST_HUMAN
2134	12022	21919		2.1	1.2E-01	BF248490.1	EST_HUMAN
2240	12124	22025		1.01	1.2E-01	AL165213.2	NT
2546	12420	22310		2.02	1.2E-01	AW996556.1	EST_HUMAN
2697	12561	22451		0.86	1.2E-01	AI623388.1	EST_HUMAN
2812	12741	22537		1.5	1.2E-01	U18018.1	NT
2872	12799	22594		1.96	1.2E-01	AI720470.1	EST_HUMAN
2904	12831	22628		2.89	1.2E-01	M16364.1	NT

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2974	12901	22700	0.98	1.2E-01	X56382.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3192	13117	23923	2	1.2E-01	AW370668.1	EST_HUMAN	QV1-BT259-261099-021-005 BT0559 Homo sapiens cDNA
3219	13143		0.97	1.2E-01	U67500.1	NT	Methanococcus jannaschii section 142 of the complete genome
3433	13350		0.79	1.2E-01	Z9918.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2795/31 to 3013540
3477	13393	23198	1.14	1.2E-01	X56382.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3477	13393	23199	1.14	1.2E-01	X56382.1	NT	Wheat mRNA for a group 3 late embryogenesis abundant protein (LEA)
3554	13350		1.2	1.2E-01	Z9918.1	NT	Bacillus subtilis complete genome (section 15 of 21); from 2795/31 to 3013540
3704	13617		0.88	1.2E-01	BF128551.1	EST_HUMAN	601810786R1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4053668 3'
4090	13990	23766	2.2	1.2E-01	Z54255.1	NT	P.clarkii mRNA; repeat region (ID 2MR17)
4090	13990	23767	2.2	1.2E-01	Z54255.1	NT	P.clarkii mRNA; repeat region (ID 2MR17)
5012	14886		1.04	1.2E-01	P16466	SWISSPROT	HEMOYSIN PRECURSOR
5174	15040	24807	1.47	1.2E-01	Q10441	SWISSPROT	HYPOTHETICAL 52.4 KD PROTEIN C12B10.08C IN CHROMOSOME 1
5174	15040	24808	1.47	1.2E-01	Q10441	SWISSPROT	HYPOTHETICAL 52.4 KD PROTEIN C12B10.08C IN CHROMOSOME 1
5199	15062		2.47	1.2E-01	AW401856.1	EST_HUMAN	UI-HF-B10-ah8-d-01-0-U1r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3053617 5'
5251	15174	24947	2.63	1.2E-01	W33035.1	EST_HUMAN	ZC080211 Soares_parathyroid_tumor_NbHPA_Homo sapiens cDNA clone IMAGE:321699 5'
5297	15218	25021	1.9	1.2E-01	Z98266.1	NT	Human gene encoding plektophillin (exons 1-13)
5762	15669	25776	1.69	1.2E-01	BE620945.1	EST_HUMAN	601403518F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3895613 5'
5806	15711	25824	2.19	1.2E-01	AW845275.1	EST_HUMAN	IL0-CT0031-22/1099-113-e04 CT0031 Homo sapiens cDNA
5839	15745	25858	1.56	1.2E-01	M26925.1	NT	Mouse galactosyltransferase mRNA, complete cds
6607	16487		1.21	1.2E-01	BE001072.1	EST_HUMAN	PM3-BN0137-290300-002-f03 BN0137 Homo sapiens cDNA
6642	16522	26715	2.46	1.2E-01	AI913753.1	EST_HUMAN	WC99g03.x1 NCI_CGAP_C68 Homo sapiens cDNA clone IMAGE:2328804 3' similar to SW_GST2_HUMAN Q39735 MICROSONAL GLUTATHIONE S-TRANSFERASE II;
6893	16772		9.72	1.2E-01	AW083652.1	EST_HUMAN	XC490107.x1 NCI_CGAP_Eso2 Homo sapiens cDNA clone IMAGE:2587597 3' similar to gblM13452 LAMIN A (HUMAN);
6904	16782		3.86	1.2E-01	AF053772.1	NT	Staphylococcus aureus plasmid pSK23 putative recombinase Sin (sin) gene, partial cds, and transcriptional regulator QacR (qacR) and multidrug efflux protein QacB (dacB) genes, complete cds
7043	16920		2.27	1.2E-01	U3214.1	NT	Haemophilus influenzae Rd section 29 of 163 of the complete genome
7521	17340	27546	1.5	1.2E-01	X77961.1	NT	S.cerevisiae HXT5 gene
7747	17597	27819	1.51	1.2E-01	AV710857.1	EST_HUMAN	AV710857 Cu Homo sapiens cDNA clone CjAAKE08 5'
8260	18140		2.95	1.2E-01	D26184.1	NT	Yeast MFT5 gene for suppressor protein, complete cds
8417	18291		3.35	1.2E-01	BE962324.2	EST_HUMAN	601665578R1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3546283 3'
8487	18360		1.93	1.2E-01	BF314481.1	EST_HUMAN	601900763F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4130103 5'
8579	18447	28715	2.6	1.2E-01	AF100493.1	NT	Human sapiens dynein intermediate chain DNA1 (DNA1) gene, exon 17

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8798	18612			2.02	1.2E-01 M65109.1	NT	Rabbit glycogen-associated protein phosphatase regulatory subunit (RG1) mRNA, complete cds
9032	18822			2.22	1.2E-01 AV658033.1	EST_HUMAN	AV658033 GLC Homo sapiens cDNA clone GLCfB12 3'
9383	19043			2.78	1.2E-01 AJ21736.1	NT	Homo sapiens Xq pseudoautosomal region, segment 2/2
9458	19693	24897		2.58	1.2E-01 Q04912	SWISSPROT (CDW136)	MACROPHAGE-STIMULATING PROTEIN RECEPTOR PRECURSOR (MSP RECEPTOR) (P185-RON)
9567	10476			7.69	1.2E-01 AF039442.1	NT	Homo sapiens colon cancer antigen NY-CO-45 mRNA, partial cds
9671	19230			1.41	1.2E-01 X53881.1	NT	R.norvegicus NFE68 gene for 68Da neurofilament
9739	19706	24903		2.36	1.2E-01 BE061418.1	EST_HUMAN	QV4BT0234-111199-031-g10 BT0234 Homo sapiens cDNA
9761	19281	25231		3.68	1.2E-01 A129903.1	EST_HUMAN	gn20g05_x1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1898840 3'
9782	19295			2.07	1.2E-01 L10187.1	NT	Xenopus laevis integrin alpha 3 subunit mRNA, partial cds
9786	19636			4.72	1.2E-01 O96433	SWISSPROT CYCLIN T	
9960	19424			2.18	1.2E-01 BF314481.1	EST_HUMAN	601900763F1 NIH MGCG 19 Homo sapiens cDNA clone IMAGE:4130103 5'
552	10493	20301	0.95	1.1E-01 A1561003.1	EST_HUMAN	tn18d08_x1 NCI_CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2167983 3'	
599	10535	20344	3.38	1.1E-01 AA569006.1	EST_HUMAN	nm08911_s1 NCI_CGAP_Cat0 Homo sapiens cDNA clone IMAGE:1059620 3' similar to gb:X06985_mai	
1038	10956	20759	1.53	1.1E-01 BF697308.1	EST_HUMAN	HEME OXYGENASE 1 (HUMAN);	
1069	10985		1.29	1.1E-01 AL161560.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 60	
1143	12686	20899	4.06	1.1E-01 AW972158.1	EST_HUMAN	EST384142 MAGE sequences, MAGL Homo sapiens cDNA	
1229	11137	20990	1.72	1.1E-01 D64004.1	NT	Synechocystis sp. PCC6803 complete genome, 23/27, 2868767-3002965	
1504	11408	24267	2.47	1.1E-01 AU140363.1	EST_HUMAN	AL140363 PLACE2 Homo sapiens cDNA clone PLACE2000403 5'	
2266	12150		2.25	1.1E-01 6755215	NT	Mus musculus pre T-cell antigen receptor alpha (Pcta), mRNA	
2492	12653		1.17	1.1E-01 6978676	NT	Rattus norvegicus Procollagen II alpha 1 (Col2a1), mRNA	
2520	12394		1.17	1.1E-01 AW821909.1	EST_HUMAN	RCO-ST0379-2/010100-032-g04 ST0379 Homo sapiens cDNA	
2825	12754	22546	1.84	1.1E-01 S82418.1	NT	interleukin-12 p65 subunit [Inr1c], Genomic, 700 nt, segment 4 of 5]	
2997	12925	22717	0.8	1.1E-01 F03265.1	EST_HUMAN	HSC1RF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1rf02 3'	
3299	13221		1.39	1.1E-01 6753231	NT	Mus musculus calcium channel, voltage-dependent, T type, alpha 1G subunit (Caenca1g), mRNA	
3374	13293	23092	3	1.1E-01 BE393186.1	EST_HUMAN	601308679F1 NIH MGCG_44 Homo sapiens cDNA clone IMAGE:3627066 5'	
3405	13322	23123	1.54	1.1E-01 X62135.1	NT	C.reinhardtii nuclear gene on linkage group XII	
3534	13450		0.94	1.1E-01 Y07895.1	NT	A.immersus gene for transposase	
3648	13562	23348	1.23	1.1E-01 X52708.1	NT	G.gallus gene encoding non-histone chromosomal protein HMG-14b, exons 4 and 5	
4021	13925	23698	1.31	1.1E-01 AW819442.1	EST_HUMAN	MR3-ST0290-280100-025-907 ST0290 Homo sapiens cDNA	
4021	13925	23699	1.31	1.1E-01 AW819442.1	EST_HUMAN	MR3-ST0290-280100-025-907 ST0290 Homo sapiens cDNA	

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Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4027	13930			0.87	1.1E-01 AF030001.1	NT	Mus musculus major histocompatibility locus class III region:butyrophilin-like protein gene, partial cds; Notch4, PBX2, RAGE, lysophatidic acid acyl transferase-alpha, palmitoyl-protein thioesterase 2 (PPT2), CREB-RP, and fensin X (TNX) genes, complex
4159	14059			7.93	1.1E-01 AF157066.1	NT	Drosophila melanogaster Marsicht protein (kar) mRNA, complete cds
4189	14089	23867		0.8	1.1E-01 AW0202056.1	EST_HUMAN	IL5-UM0070-0202050-068-a08 UM0070 Homo sapiens cDNA
4466	14360	24150		0.91	1.1E-01 AF064564.2	NT	Fugu rubripes neurofibromatosis type 1 (NF1), A-kinase anchor protein (AKAP84), BAW protein (BAW), and WSB1 protein (WSB1) genes, complete cds
4539	14432	24214		2.02	1.1E-01 S44957.1	NT	Tapa-1=Integral membrane protein TAPA-1 [mice, B cell lymphoma line 38C13, Genomic, 1973 nt, segment 1 of 7]
4725	14611	24397		1.26	1.1E-01 Y07895.1	NT	A_immersus gene for transposase
4819	14702	24487		1.25	1.1E-01 D90308.1	NT	Synechocystis sp. PCC6803 complete genome, 10/27, 1188886-1311234
5479	15399			1.43	1.1E-01 AA747216.1	EST_HUMAN	mx76a03.s1 NCI_CGAP_Ewi Homo sapiens cDNA clone IMAGE:1268140 similar to contains Alu repetitive element; contains element MER35 repetitive element;
5662	15478	25551		1.54	1.1E-01 X68851.1	NT	S_pombe ste8 gene encoding protein kinase
5579	15494	25570		4.73	1.1E-01 M86533.1	NT	Providencia rettgeri penicillin G amidase gene
5672	15581	25681		1.46	1.1E-01 AJ007973.1	NT	Homo sapiens LGMD2B gene
6687	15596	25697		1.79	1.1E-01 BE769152.1	EST_HUMAN	PM3-FT024-130600-004-f12 FT0024 Homo sapiens cDNA
5697	15606	25708		7.01	1.1E-01 AW853689.1	EST_HUMAN	RC3-CT0254-280893-01-01-a01 CT0254 Homo sapiens cDNA
5876	15782	25903		1.39	1.1E-01 AF035746.1	EST_HUMAN	AF035746 Human salivary gland cell line HSG Homo sapiens cDNA clone RL43
5985	15890	26012		3.48	1.1E-01 O69385	SWISSPROT	ACETYL-COENZYME A SYNTHETASE (ACETATE--COA LGASE) (ACYL-ACTIVATING ENZYME)
6027	15931			2.9	1.1E-01 AF032922.1	NT	Homo sapiens syntaxis 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds
6068	16052	26198		2.21	1.1E-01 11432372	NT	Homo sapiens phosphatidylinositol glycan, class B (PIGB) mRNA
6448	16309	26474		7.05	1.1E-01 BF64628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019_5'
6448	16309	26475		7.05	1.1E-01 BF64628.1	EST_HUMAN	602140976F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4302019_5'
6513	16372	26550		1.74	1.1E-01 P41067	SWISSPROT	TRAB PROTEIN
6531	16390	26570		3.07	1.1E-01 AA738784.1	EST_HUMAN	eh31b06.s1 Soares_pariathyroid_tumor_NbHPA_Homo sapiens cDNA clone 1240403 3' similar to gb:J03483 CHROMOGRANIN A PRECURSOR (HUMAN);
6777	16656	26845		1.57	1.1E-01 AA493574.1	EST_HUMAN	rh04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
6777	16656	26846		1.57	1.1E-01 AA493574.1	EST_HUMAN	rh04g10.s1 NCI_CGAP_Thy1 Homo sapiens cDNA clone IMAGE:943362
6803	16682	26872		1.22	1.1E-01 X91233.1	NT	H_sapiens IL15 gene
6826	16705			1.24	1.1E-01 AW817918.1	EST_HUMAN	PM1-ST0270-050200-001-f09 ST0270 Homo sapiens cDNA
6862	16741	26834		1.78	1.1E-01 AL134349.1	EST_HUMAN	DKFZp547P194_r1_547 (synonym: hb1r1) Homo sapiens cDNA clone DKFZp547P194_5'
7118	16995	27186		2.19	1.1E-01 U02482.1	NT	Pediococcus acidilactici H plasmid pSMB74 pediocin AcH production (pap) gene cluster papA, papB, papC and papD genes, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7228	17105	27294		2.24	1.1E-01 AA192153.1	EST_HUMAN	zp93b12_r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:6277743 5'
7228	17105	27295		2.24	1.1E-01 AA192153.1	EST_HUMAN	zp93b12_r1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:6277743 5'
7287	17163	27362		2.48	1.1E-01 T72675.1	EST_HUMAN	YD19n03_s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:108725 3' similar to gb:M81181 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-2 (HUMAN);
7467	17327			2.08	1.1E-01 BF035149.1	EST_HUMAN	MR2_GN0027-046900-005-008 GN0027 Homo sapiens cDNA
7861	17711			1.23	1.1E-01 R80590.1	EST_HUMAN	y96ad09_s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:147064 3'
8181	12925	22717		1.94	1.1E-01 F03265.1	EST_HUMAN	HSCTRF022 normalized infant brain cDNA Homo sapiens cDNA clone c-1tf022 3'
8294	18173			3.88	1.1E-01 AF169032.1	NT	Carassius auratus activin beta A precursor, mRNA, complete cds
8402	18278	28530		2.93	1.1E-01 R23708.1	EST_HUMAN	Yh35f12_r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131759 5' similar to contains Alu repetitive element; contains TAR1 repetitive element;
8519	18391	28655		1.85	1.1E-01 X70058.1	NT	M.musculus cytokine gene
8539	18411	28676		3.21	1.1E-01 Z1910.1	NT	Z.mobilis tgf and lig genes encoding tRNA guanine transglycosylase and DNA ligase
8539	18411	28677		3.21	1.1E-01 Z1910.1	NT	Z.mobilis tgf and lig genes encoding tRNA guanine transglycosylase and DNA ligase
8626	18491	28763		2.79	1.1E-01 P17437	SWISSPROT	SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)
9241	18956			3.19	1.1E-01 BE767023.1	EST_HUMAN	RC2-NT0112-120600-014-003 NT0112 Homo sapiens cDNA
9485	19507			2.06	1.1E-01 BE974556.1	EST_HUMAN	601630551R2 NIH MGC 83 Homo sapiens cDNA clone IMAGE:3950604 3'
9893	19372	25792		2.14	1.1E-01 BF239753.1	EST_HUMAN	601606350F1 NIH MGC 54 Homo sapiens cDNA clone IMAGE:4134085 5'
1183	11094			4.08	1.0E-01 O62855	SWISSPROT	DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)
1251	11158	241007		1.89	1.0E-01 A1985499.1	EST_HUMAN	WS08d01_x1 NCL CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2486577 3' similar to contains MERT7.13 MERT7 repetitive element;
1370	11276	21132		2.88	1.0E-01 AL161504.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 16
2439	12316	22213		1	1.0E-01 AW451365.1	EST_HUMAN	U1-H-B13-acd-07-0-U1_s1 NCL CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736420 3'
3468	13384	23189		0.98	1.0E-01 BF038991.1	EST_HUMAN	601456301F1 NIH MGC_66 Homo sapiens cDNA clone IMAGE:3859849 5'
3658	13572	23359		1.01	1.0E-01 BF299818.1	EST_HUMAN	601906489F1 NIH MGC_54 Homo sapiens cDNA clone IMAGE:4134071 5'
3871	13782	23874		2.44	1.0E-01 BF358703.1	EST_HUMAN	QV2-NT0048-160800-316-e05 NT0048 Homo sapiens cDNA
4307	14204	23987		1.5	1.0E-01 AE02265.2	NT	Chlamydophila pneumoniae AR39, section 91 of 94 of the complete genome
4455	14349			1.17	1.0E-01 A1792349.1	EST_HUMAN	en3204.y5 Geesler Wilms tumor-Homo sapiens cDNA clone IMAGE:1700353 5
4613	14501	24289		1.26	1.0E-01 U50460.1	NT	Drosophila melanogaster tyrosine kinase p45 isoform (fey) mRNA, complete cds
4638	14719			2.06	1.0E-01 AW652344.1	EST_HUMAN	EST364414 MAGE resequences, MAGB Homo sapiens cDNA
5158	15025	24792		0.87	1.0E-01 D49683.1	NT	Mouse FIZ2_F1 gene
5188	15051	24815		1.44	1.0E-01 BF515935.1	EST_HUMAN	U1-H-BW1-act-e-12-0-U1_s1 NCL CGAP_Sub7 Homo sapiens cDNA clone IMAGE:3084023 3'
5260	15182			9.16	1.0E-01 W86490.1	EST_HUMAN	Zh62104_s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:418695 3'
5670	15580	25680		11.21	1.0E-01 AF274875.1	NT	Homo sapiens growth factor receptor-bound protein 7 (GRB7) gene, complete cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6187	16072		1.88	1.0E-01	R23821.1	EST_HUMAN	yf34h06_r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:131675 5' similar to contains Alu repetitive element;
6549	16407		2.45	1.0E-01	Y12488.1	NT	M.musculus whn gene
7299	17175	27376	1.16	1.0E-01	AF102855.2	NT	Rattus norvegicus synaptic SAPAP3-interacting protein Synanon mRNA, complete cds
7473	17933		1.8	1.0E-01	M76729.1	NT	Human pro-alpha-1 (V) collagen mRNA, complete cds
7505	17293		2.73	1.0E-01	AE001501.1	NT	Helicobacter pylori, strain J99 section 62 of 132 of the complete genome
7651	17501	27724	1.84	1.0E-01	BF240154.1	EST_HUMAN	6019056_61/F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4133487 5'
7713	17563	27788	9.08	1.0E-01	AB046799.1	NT	Human sapiens mRNA for KIAA1579 protein, partial cds
7713	17563	27789	9.08	1.0E-01	AB046799.1	NT	Human sapiens mRNA for KIAA1579 protein, partial cds
7918	17768	28007	1.26	1.0E-01	BE792750.1	EST_HUMAN	6015846_604/F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3939096 5'
8050	17941		2.02	1.0E-01	AU159127.1	EST_HUMAN	AU159127/THYRO1 Homo sapiens cDNA clone THYRO1000895 3'
8393	18269	28520	2.9	1.0E-01	BF242846.1	EST_HUMAN	6018777_03/F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
8393	18269	28521	2.9	1.0E-01	BF242846.1	EST_HUMAN	6018777_03/F1 NIH_MGC_55 Homo sapiens cDNA clone IMAGE:4106089 5'
8703	18521	28503	4.43	1.0E-01	BE760543.1	EST_HUMAN	6015825_58/F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936734 5'
9226	19285		2.5	1.0E-01	BE5317719.1	EST_HUMAN	6010685_554/F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451983 5'
9453	19085		1.34	1.0E-01	7682165	NT	Human sapiens KIAA0514 gene product (KIAA0514), mRNA
9469	19098		2.03	1.0E-01	X00854.1	NT	Drosophila melanogaster fiz gene
9735	19688		2.57	1.0E-01	U52691.1	NT	Gonyaulax polyedra putative type-1 serine/threonine phosphatase (PP1) mRNA, complete cds
9765	19285		2.46	1.0E-01	BE5317719.1	EST_HUMAN	6010685_554/F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451983 5'
9818	19664		8.59	1.0E-01	U68384.1	NT	Saccharomyces cerevisiae suppressor of ABF1 (SAB2) gene, complete cds
9871	19360	25187	1.28	1.0E-01	AJ271049.1	NT	Zea mays mRNA for Tic34-2 protein (tic34B gene)
9877	19363		4.16	1.0E-01	AF001507.1	NT	Bacillus halodurans genomic DNA, section 1/14
							Drosophila melanogaster cAMP-dependent protein kinase type II regulatory subunit (pka-RII) mRNA, complete cds
2752	12614	22505	1.09	9.9E-02	AF274008.1	NT	
2752	12619	22511	1.44	9.9E-02	BE545554.1	EST_HUMAN	6010702_19/F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
2757	12619	22512	1.44	9.9E-02	BE545554.1	EST_HUMAN	6010702_19/F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3456365 5'
2950	12877	22675	0.92	9.9E-02	AV730747.1	EST_HUMAN	AV730747/HTFBND05 5'
3229	13153	22952	1.15	9.9E-02	AF098810.1	NT	Human sapiens neuretin III alpha gene, partial cds
4582	14472	24260	22.55	9.9E-02	BE674249.1	EST_HUMAN	7d77c12/x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278998 3'
6161	15118	24862	7.96	9.9E-02	D83710.1	NT	Aspergillus terreus BSD mRNA for blasticidin S deaminase, complete cds
7332	17236	27440	1.5	9.9E-02	6755111	NT	Mus musculus phospholipid transfer protein (Plip), mRNA
551	10492		1.58	9.8E-02	X56388.1	NT	O.sativa R-amy3C gene for alpha-amylase
1711	11612	21482	1.53	9.8E-02	4503224	NT	Human sapiens cytochrome P450, subfamily IIIf, polypeptide 1 (CYP2E1) mRNA
3106	13032	22827	3.28	9.8E-02	AF134274.1	NT	Daucus carota leucanthothiocyanidin dioxygenase 2 (LDOX) mRNA, LDOX-2 allele, complete cds

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
4131	14031	23805	6.67	9.8E-02	AF257329.1	NT	Leptospira macularis beta-tubulin mRNA, complete cds
4131	14031	23806	6.67	9.8E-02	AF257329.1	NT	Leptospira macularis beta-tubulin mRNA, complete cds
8755	17904	28148	2.1	9.8E-02	BF037421.1	EST_HUMAN	601460793r1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3384237 5'
1328	11235	21092	1.16	9.7E-02	AB05608.1	NT	Aloe arborescens mRNA for NADP-malic enzyme, complete cds
1567	11471		0.98	9.7E-02	4503710	NT	Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3) mRNA
2214	12100	22004	2.37	9.7E-02	BE166860.1	EST_HUMAN	QV1-HT0516-070300-095-a04 HT0516 Homo sapiens cDNA CELL SURFACE A33 ANTIGEN PRECURSOR (GLYCOPROTEIN A33)
3901	13811		3.56	9.7E-02	Q89795	SWISSPROT	EST366546 MAGE resequences, MAGC Homo sapiens cDNA
5661	15572	25669	1.39	9.7E-02	AW54476.1	EST_HUMAN	EST366546 MAGE resequences, MAGC Homo sapiens cDNA
6321	16184	26345	4.27	9.7E-02	Z99119.1	NT	Bacillus subtilis complete genome (Section 16 of 21). From 2897771 to 3213410
6655	16535	26731	1.59	9.7E-02	N22798.1	EST_HUMAN	yw41cd3s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:2547988 3'
6655	16535	26732	1.59	9.7E-02	N22798.1	EST_HUMAN	yw41cd3s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:2547988 3'
7137	17014	27207	1.32	9.7E-02	AI853984.1	EST_HUMAN	wx78p06.x1 NCL_CGAP_Ov38 Homo sapiens cDNA clone IMAGE:2549747 3' similar to gb:X52851_maf1
8531	18403		1.97	9.7E-02	U58337.1	NT	Mus musculus Igf1 (Igfb1) mRNA, partial cds
1969	11862	21753	1.27	9.6E-02	AI080721.1	EST_HUMAN	0247d11x1 Soares_NHNMPr_u_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
1969	11862	21754	1.27	9.6E-02	AI080721.1	EST_HUMAN	0247d11x1 Soares_NHNMPr_u_S1 Homo sapiens cDNA clone IMAGE:1678485 3'
4248	14147	23921	6.02	9.6E-02	Z32086.2	NT	Proteus mirabilis fimbrial operon, strain HI4320
4932	14810	24879	0.94	9.6E-02	AW066230.1	EST_HUMAN	EST378303 MAGE resequences, MAGI Homo sapiens cDNA
5093	14963	24738	0.8	9.6E-02	BE0361729.1	EST_HUMAN	RC5-BT0254-031090-01-a03 BT0254 Homo sapiens cDNA
5713	15621		2.72	9.6E-02	BE910039.1	EST_HUMAN	601498088r1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3900165 5'
7502	17371	27580	1.51	9.6E-02	AV687898.1	EST_HUMAN	AV687898 GKC Homo sapiens cDNA clone GKCRAH02 5'
7677	17527		1.84	9.6E-02	BE894895.1	EST_HUMAN	601434080r1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3919363 5'
7772	17622	27855	1.75	9.6E-02	AJ24211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
7772	17622	27856	1.75	9.6E-02	AJ24211.1	NT	Homo sapiens DMBT1 candidate tumour suppressor gene, exons 1 to 55
7839	17689	27833	1.59	9.6E-02	AB013985.1	NT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
7839	17689	27834	1.59	9.6E-02	AB013985.1	NT	Antirrhinum majus transposon Tam3 pseudogene for transposase (in S-5 copy)
7886	17736	27980	3.29	9.6E-02	P08174	SWISSPROT	COMPLEMENT DEGRADATION FACTOR PRECURSOR (CD55)
8125	18013	28260	6.51	9.6E-02	Z79102.1	NT	Mycobacterium tuberculosis H37Rv complete genome, segment 102/162
8857	18764	29056	1.8	9.6E-02	AA625755.1	EST_HUMAN	zug9101.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:745392 3'
9798	19312		1.38	9.6E-02	H14599.1	EST_HUMAN	ym19n03.s1 Soares_infant brain 1N1B Homo sapiens cDNA clone IMAGE:48653 3'
9848	19344	25212	1.26	9.6E-02	BE728219.1	EST_HUMAN	601563335r1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832908 5'
4012	13918	23894	2.25	9.5E-02	AW992395.1	EST_HUMAN	CN2-BN0023-050200-087-f12 BN0023 Homo sapiens cDNA
5062	14932	24704	0.87	9.5E-02	U63374.1	NT	Lyopersicon esculentum polygalacturonase isoenzyme 1 beta subunit gene, complete cds

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6323	16186	26348	3.72	9.5E-02	AB03473.1	NT	Trimeresurus flavoviridis DNA for phospholipase A2 inhibitor, complete cds
6467	16527	26494	7.46	9.5E-02	AL161538.2	NT	Arribidopsis thaliana DNA chromosome 4, contig fragment No. 38
6599	16479	26666	2.59	9.5E-02	BF035861.1	EST_HUMAN	6011453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
6599	16479	26667	2.59	9.5E-02	BF035861.1	EST_HUMAN	6011453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
8066	17957	28206	3.29	9.5E-02	BF035861.1	EST_HUMAN	6011453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
8066	17957	28207	3.29	9.5E-02	BF035861.1	EST_HUMAN	6011453642F1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3857243 5'
1792	11690	21665	3.86	9.4E-02	BF671063.1	EST_HUMAN	60215082F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4291917 5'
1820	11717	21597	0.86	9.4E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
1820	11717	21598	0.86	9.4E-02	U55944.1	NT	Cavia porcellus 3beta-hydroxysteroid sulfotransferase mRNA, complete cds
3804	13718	23504	4.34	9.4E-02	Z33059.1	NT	M.capricolum DNA for CONTTG MC073
4980	14855	24621	0.89	9.4E-02	6753517	NT	Mus musculus coding region determinant-binding protein (Crdbp), mRNA
6999	16876		2.62	9.4E-02	Z46563.1	NT	Acinetobacter sp. cysD, cobQ, sodM, lysS, rubB, estB, oxyR, ppk, mtgA, ORF2 and ORF3 genes
8304	16338	26505	2.69	9.4E-02	L78333.1	NT	Human ERCA1, Rho7 and vati genes, complete cds, and ip25 gene, partial cds
9083	19603		3.36	9.4E-02	U31815.1	NT	Rattus norvegicus calcium channel alpha-1C subunit (ROB2) mRNA, partial cds
9843	19411	25182	1.42	9.4E-02	U27699.1	NT	Human peptGBT-1 betaine-GABA transporter mRNA, complete cds
2860	12887		1.83	9.3E-02	4809280	NT	Human sapiens BA11-associated protein 3 (BA1AP3) mRNA
2893	12921		5.39	9.3E-02	69112825	NT	Human sapiens nasopharyngeal epithelium specific protein 1 (NESG1), mRNA
3218	13142	22946	2.03	9.3E-02	BF575511.1	EST_HUMAN	602153086F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4288269 5'
4060	13962	23738	3.51	9.3E-02	BE391943.1	EST_HUMAN	60112860182F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3807653 5'
4060	13962	23739	3.51	9.3E-02	BE391943.1	EST_HUMAN	60112860182F1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3807653 5'
4628	14516		1.88	9.3E-02	AV732224.1	EST_HUMAN	AV732224 HTF Homo sapiens cDNA clone HTFAUA06 5'
7599	17450	27665	2.24	9.3E-02	BE962631.2	EST_HUMAN	6016559988R1 NIH_MGC_66 Homo sapiens cDNA clone IMAGE:3855981 3'
7855	17705	27949	3.52	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
7855	17705	27950	3.52	9.3E-02	Q15034	SWISSPROT	HYPOTHETICAL PROTEIN KIAA0032
7913	17763		3.74	9.3E-02	AW206117.1	EST_HUMAN	U1-H-B1-afx-h-05-0-U1-s1 NC1_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2723553 3'
9343	19527		1.85	9.3E-02	AJ249850.1	NT	Photobacterium damseliae subsp. damseliae partial gyB gene for DNA gyrase B subunit
9704	19555		8.62	9.3E-02	AW468850.1	EST_HUMAN	hg28h12x1 Scarees_NEL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2910887 3'
9896	19602		1.95	9.3E-02	AF100956.1	NT	Mus musculus major histocompatibility locus class II region; Fas-binding protein Daxx (DAXX) gene, partial cds; BING1 (BING1), tapasin (tapasin), RalGDS-like factor (RLF), KE2 (KE2), BING4 (BING4), betai, 3-galactosyl transferase (beta1,3-galactosyl tr->
228	10197	20008	4.32	9.2E-02	U60355.1	NT	Molluscum contagiosum virus subtype 1, complete genome
228	10197	20009	4.32	9.2E-02	U60355.1	NT	Molluscum contagiosum virus subtype 1, complete genome
228	10197	20010	4.32	9.2E-02	U60355.1	NT	Molluscum contagiosum virus subtype 1, complete genome

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2180	12067			2.2	9.2E-02 R54156.1	EST_HUMAN	Y98807.1 Soares infant brain [NIB Homo sapiens cDNA clone IMAGE:41618 5'
3142	13067	22866		4.53	9.2E-02 Q28631	SWISSPROT	MAJOR EPIDIDYMIS SPECIFIC PROTEIN E4 (EPIDIDYMAL PROTEIN BE-20)
3265	13188	22986		1.16	9.2E-02 AA534354.1	EST_HUMAN	nt79e01.s1 NCL_CGAP_Co3 Homo sapiens cDNA clone IMAGE:926136 3'
3537	13453			1.12	9.2E-02 6755215 NT		Mus musculus pre T-cell antigen receptor alpha (Pcrα), mRNA
4145	14045			1.34	9.2E-02 U92048.1	NT	Human herpesvirus 1 strain KOS-63, latency-associated transcript, promoter region
4211	14109			1.02	9.2E-02 BE299722.1	EST_HUMAN	6009443-65F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:2960176 5'
4538	14431	24213		1.86	9.2E-02 X96402.1	NT	G. gallus Mia-CK gene
6670	16550	26746		1.86	9.2E-02 T49920.1	EST_HUMAN	ye99c09.1 Stratagene placenta (#327225) Homo sapiens cDNA clone IMAGE:689808 5' similar to similar to gb:X566009 GUANINE NUCLEOTIDE-BINDING PROTEIN G(S), ALPHA SUBUNIT (HUMAN)
6756	16635	26823		2.07	9.2E-02 X95256.1	NT	H.vulgaris xylose isomerase gene
417	9984	19776		2.77	9.1E-02 X77695.1	NT	O. cuniculus k12 keratin gene
2385	12245	22139		1.01	9.1E-02 P78395	SWISSPROT	6-PHOSPHOFRUCTOKINASE (PHOSPHOHEXOKINASE)
3618	13532			1.14	9.1E-02 AW372569.1	EST_HUMAN	PM2-BT0349-161-289-001-02 BT0349 Homo sapiens cDNA
4583	14279	24058		1.81	9.1E-02 AL161554.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 54
							Homo sapiens MSH5 gene, partial cds; and CLIC1, DDAH, G6b, G6c, G6d, G6e, G6f, BAT5, G6b, CSK2B, BAT4, G4, Apo M, BAT3, BAT2, AIF-1, 1C7, LST-1, LTB, TNF, and LT genes, complete cds
5507	15425	25487		1.73	9.1E-02 AF129756.1	NT	au74a05 Y1 Schneider fetal brain 00004 Homo sapiens cDNA clone IMAGE:27819863 5'
6372	16234	26393		11.89	9.1E-02 AW760658.1	EST_HUMAN	FB19F10 Fetal brain, Stratagene Homo sapiens cDNA clone FB19F10 3' end
7958	17808			1.65	9.1E-02 T02984.1	EST_HUMAN	Bacteriophage Mu, complete genome
9021	18815			1.29	9.1E-02 9633494 NT		zp38h12_s1 Stratagene muscle 937209 Homo sapiens cDNA clone IMAGE:611783 3' similar to SW:TRT3_HUMAN P45378 TROPONIN T, FAST SKELETAL MUSCLE, ISOFORM BETA;
9256	19692			1.52	9.1E-02 AA1798901.1	EST_HUMAN	Hom sapiens partial MUC3B gene for MUC3B mucin, exons 1-11
9785	19548			5.63	9.1E-02 AJ291390.1	NT	FOLATE RECEPTOR ALPHA PRECURSOR (FR-ALPHA) (FOLATE RECEPTOR 1) (FOLATE RECEPTOR, ADULT) (ADULT FOLATE-BINDING PROTEIN) (FBP) (OVARIAN TUMOR-ASSOCIATED ANTIGEN MOV18) (KB CELLS FBP)
727	10659	20490		3.36	9.0E-02 P15328	SWISSPROT	hv39g10_x1 NCL_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3175842 3' similar to contains Alu repetitive element
1617	11521	21379		6.45	9.0E-02 BE220482.1	EST_HUMAN	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
2772	12634	22628		1.11	9.0E-02 AF138522.1	NT	HIV-1 p8c095-06 from USA envelope glycoprotein (env) gene, partial cds
2772	12634	22629		1.11	9.0E-02 AF138522.1	NT	Dicthyostelium discoideum spore coat structural protein SP65 (cotE) gene, complete cds
3294	13216	23018		0.92	9.0E-02 AF270135.1	NT	corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4202	14101	23893		0.8	9.0E-02 S68757.1	NT	corticosteroid-binding globulin [Saimiri sciureus=squirrel monkeys, liver, mRNA, 1474 nt]
4202	14101	23884		0.8	9.0E-02 S68757.1	NT	LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ)
4321	14218	24001		1.2	9.0E-02 P55268	SWISSPROT	

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4568	14460	24248		1.79	9.0E-02 X65740.2	NT	Plasmidium falcatum P-type ATPase 3 gene
5142	15009	24780		1.06	9.0E-02 Q24597	SWISSPROT	REGULATORY PROTEIN ZESTE
5647	15560	25653		8.02	9.0E-02 W56037.1	EST_HUMAN	Zag68a12.1r1 Soares_fetal_lung_NbHL19W Homo sapiens cDNA clone IMAGE:297694.5 similar to PIR:552171 S52171 small G protein - human ;
9967	19428			15.35	9.0E-02 11431799 NT	EST_HUMAN	Homo sapiens chromosome 16 open reading frame 5 (C16orf5), mRNA
1419	11325	21189		2.15	8.9E-02 BF701593.1	EST_HUMAN	602128030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951.5
1419	11325	21190		2.15	8.9E-02 BF701593.1	EST_HUMAN	602128030F2 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4285951.5
2338	12218	22117		1.41	8.9E-02 BE153572.1	EST_HUMAN	PM0-HT0339-251199-003-d01 HT0339 Homo sapiens cDNA
4104	14004			1.71	8.9E-02 AF286055.1	NT	Arthrum angustatum AttranF02 protein (AttranF02) gene, partial cds
4534	14427	24208		0.92	8.9E-02 AA424887.1	EST_HUMAN	Zn03d04.s1 Soares_NhMPu_S1 Homo sapiens cDNA clone IMAGE:768199.3
5569	15485	25559		3.3	8.9E-02 AW452122.1	EST_HUMAN	U1-H-B13-alu-f-08-0-U1s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068284.3
5569	15485	25560		3.3	8.9E-02 AW452122.1	EST_HUMAN	U1-H-B13-alu-f-08-0-U1s1 NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:3068284.3
5576	15491	25568		3.13	8.9E-02 11433478 NT	EST_HUMAN	Homo sapiens similar to endoglycan (H. sapiens) (LOC63107), mRNA
6270	16135	26290		1.56	8.9E-02 P47259	SWISSPROT	FOLD BIFUNCTIONAL PROTEIN [INCLUDES: METHYLENETETRAHYDROFOLATE DEHYDROGENASE ; METHYLENETETRAHYDROFOLATE CYCLOHYDROLASE]
6460	16320			1.83	8.9E-02 Z79221.1	NT	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20f8
6998	16875	27066		5.28	8.9E-02 AA303319.1	EST_HUMAN	EST180187 Liver, hepatocellular carcinoma Homo sapiens cDNA 5' end
9228	18949			4.03	8.9E-02 BF696918.1	EST_HUMAN	602129682F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4286180.5
1351	11257	21113		1.25	8.8E-02 Q27474	SWISSPROT	PROBABLE DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE [ATP])
3828	13740	23532		0.96	8.8E-02 AA299128.1	EST_HUMAN	EST11585 Uterus Homo sapiens cDNA 5' end
3948	13856			3.24	8.8E-02 000268	SWISSPROT	TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT (TAFII-135) (TAFII135) (TAFII-130)
4205	14104			1.13	8.8E-02 4580423 NT	EST_HUMAN	Homo sapiens paired box gene 6 (antidila, keratins) (PAX6), isoform b, mRNA
7195	17072	27260		1.83	8.8E-02 AA151872.1	EST_HUMAN	Zn99a05.s1 Strategene colon #937204 Homo sapiens cDNA clone IMAGE:5652288.3
8461	18334	28596		3.19	8.8E-02 BE284455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:35355648.5
8461	18334	28597		3.19	8.8E-02 BE284455.1	EST_HUMAN	601191770F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:35355648.5
8585	18453	28722		10.63	8.8E-02 AL040129.1	EST_HUMAN	DKFZp434D1313_r1434 (synonym: htes3), Homo sapiens cDNA clone DKFZp434D1313.5
9502	19001	25532		1.38	8.8E-02 Z71561.1	NT	S.cerevisiae chromosome XIV reading frame ORF YNL285w
3636	13550	23337		3.02	8.7E-02 U82395.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds
3636	13550	23338		3.02	8.7E-02 U82395.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds

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3879	13790	23578	0.82	8.7E-02	W87844.1	EST_HUMAN	2h68a02.r1 Seares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:4171945 similar to contains element MER12 repetitive element;
4609	14497	24286	1.22	8.7E-02	AF175636.1	NT	Mus musculus JNK interacting protein-3a (Jip3) mRNA, complete cds
5034	14906		1.06	8.7E-02	AE000895.1	NT	Methanobacterium thermoautotrophicum from bases 1176181 to 1188406 (section 101 of 148) of the complete genome
5255	15177	24951	5.41	8.7E-02	AA286875.1	EST_HUMAN	2555g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:7014383
5255	15177	24952	5.41	8.7E-02	AA286875.1	EST_HUMAN	2555g08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:7014383
8094	17985		2.58	8.7E-02	LO4758.1	NT	Oryctolagus cuniculus cytochrome P-450 (CYP4A4) gene, 5' end
8631	18496	28770	1.77	8.7E-02	AJ007763.1	NT	Glucorobacter oxydans tRNA-ile and tRNA-Ala genes
9293	18994		2.58	8.7E-02	X1716.1	NT	Human DNA for immunoglobulin alpha heavy chain from a case of alpha heavy chain disease
9484	19105		1.81	8.7E-02	6679057	NT	Mus musculus nitrogen 2 (Nid2) mRNA
1232	11139	20991	7.05	8.6E-02	AJ217136.1	NT	Homo sapiens Xq pseudautosomal region; segment 212
2197	12084	21986	2.22	8.6E-02	BE403667.1	EST_HUMAN	601304016F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:36338643 5
3151	13076	22876	2.94	8.6E-02	LO5468.1	NT	Trichomonas vaginalis beta-tubulin (btub1) gene, complete cds
3593	13507		3.07	8.6E-02	AF133362.1	NT	Dicystostelium discoideum adenyl cyclase (acrA) gene, complete cds
4385	14281	24060	0.87	8.6E-02	U68179.1	NT	Oryctolagus cuniculus galactin-3 gene, untranslated exon and 5' flanking region
5708	15616	25718	4.38	8.6E-02	Y10326.1	NT	Homo sapiens LCN16 gene
5846	15752	25667	1.51	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
5846	15752	25668	1.51	8.6E-02	J00440.1	NT	Mouse germline IgM chain gene, D region; D-q52, mu switch region (part a)
6628	16508	26695	1.26	8.6E-02	5730066	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
6628	16508	26696	1.26	8.6E-02	5730066	NT	Homo sapiens Snf2-related CBP activator protein (SRCAP) mRNA
8315	18192	28441	1.98	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
8315	18192	28442	1.98	8.6E-02	AF206551.1	NT	Lacerta media cytochrome c oxidase subunit 1 gene, partial cds; mitochondrial gene for mitochondrial product
8574	18442	28710	3.63	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5
8574	18442	28711	3.63	8.6E-02	BF305606.1	EST_HUMAN	601893437F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4139216 5
8738	17887	28131	4.71	8.6E-02	AE001073.1	NT	Archaeoglobus fulgidus section 34 of 172 of the complete genome
8868	18670	28958	1.73	8.6E-02	AF238660.1	NT	Bacillus stearothermophilus BstF1 methylase (FIM) and BstF1 restriction endonuclease (FIR) genes, complete cds
2347	12227	22124	2.87	8.5E-02	AE000652.1	NT	Helicobacter pylori 26695 section 130 of 134 of the complete genome
5650	15419		1.8	8.5E-02	PR0809	SWISSPROT	M PROTEIN SEROTYPE 6 PRECIPITOSOR
5658	15570	25665	5.34	8.5E-02	AF238885.1	NT	Mus musculus phospholipase C-like protein mRNA, partial cds
7003	16880	27072	1.93	8.5E-02	6754779	NT	Mus musculus myosin XV (Myo15) mRNA

Table 4
Single Exon Probes Expressed in Heart

Probe SEQ ID NO.	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7661	17511	27737		3.07	8.5E-02 BE833054.1	EST_HUMAN	RC4-OT0037-200700-01-005 OT0037 Homo sapiens cDNA
7661	17511	27738		3.07	8.5E-02 BE833054.1	EST_HUMAN	RC4-OT0037-200700-01-005 OT0037 Homo sapiens cDNA
8396	18369			11.15	8.5E-02 AF155510.1	NT	Homo sapiens heparanase precursor; mRNA, complete cds
8512	18384	28649		4.07	8.5E-02 AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
9881	19488			1.39	8.5E-02 AJ005586.1	NT	Antirrhinum majus mRNA for MYB-related transcription factor
9841	19339			3.28	8.5E-02 AA362934.1	EST_HUMAN	EST72756 Ovary II Homo sapiens cDNA 5' end
2632	12728	22991		4.24	8.4E-02 W68330.1	EST_HUMAN	2d44e11.1 Soares_fetal_heart_NbH19W Homo sapiens cDNA clone IMAGE:343532 5'
5253	15175	24949		7.82	8.4E-02 BE267153.1	EST_HUMAN	601190436F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3554393 5'
6019	15923	26053		1.71	8.4E-02 AK024458.1	NT	Homo sapiens mRNA for FLJ00050 protein, partial cds
6680	16560	26755		8.11	8.4E-02 BE095074.1	EST_HUMAN	CM3-BT0730-260400-162-005 BT0790 Homo sapiens cDNA
7931	17781	28020		1.44	8.4E-02 AI735184.1	EST_HUMAN	as88g10.1x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2335842 3' similar to TR:Q88312
1965	11859	21748		0.86	8.3E-02 5635680	NT	Ixodes hexagonus mitochondrial, complete genome
1965	11859	21749		0.86	8.3E-02 5635680	NT	Ixodes hexagonus mitochondrial, complete genome
3544	13460	23254		6.19	8.3E-02 P75334	SWISSPROT	HYPOTHETICAL LIPOPROTEIN MG309 HOMOLOG PRECURSOR
3567	13481	23271		0.88	8.3E-02 AI436797.1	EST_HUMAN	th82g06.X1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
3567	13481	23272		0.88	8.3E-02 AI436797.1	EST_HUMAN	th82g06.X1 Soares_NHMPU_S1 Homo sapiens cDNA clone IMAGE:2125210 3'
5840	15746	25659		2.82	8.3E-02 AF0526683.1	NT	Homo sapiens protocadherin 43 gene, exon 1
6653	16533	26728		3.42	8.3E-02 AF1982787.1	NT	Rattus norvegicus dystrophin-related protein 2 A-form splice variant (Drp2) mRNA, complete cds
6871	16551			1.47	8.3E-02 AA865285.1	EST_HUMAN	cg88g08_s1 NCI_CGAP_Kids Homo sapiens cDNA clone IMAGE:14554122 3' similar to contains L111 L111 repetitive element;
6829	16708			1.42	8.3E-02 AA987873.1	EST_HUMAN	cq81f10_s1 NCI_CGAP_Kids Homo sapiens cDNA clone IMAGE:1582779 3'
7498	17368	27573		1.44	8.3E-02 AM583503.1	EST_HUMAN	SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE ;
7506	17294			1.94	8.3E-02 AL161595.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 91
9207	19695			1.55	8.3E-02 BE953458.1	EST_HUMAN	6016a4770F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:3929993 5'
1357	11263			7.82	8.2E-02 Y08170.2	NT	Gallus gallus mRNA for OBCAM protein gamma isoform
1480	11385	21248		1.21	8.2E-02 AF167077.2	NT	Canis familiaris glutamate transporter (EAAT4) mRNA, complete cds
3036	12964			1.78	8.2E-02 AL168206.2	NT	Homo sapiens chromosome 21 segment HS21C006
3733	13645			1.26	8.2E-02 AL161498.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 10
3926	13835	23615		1.11	8.2E-02 AL168206.2	NT	Homo sapiens chromosome 21 segment HS21C006
4187	14087	23862		5.36	8.2E-02 P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4187	14087	23863		5.36	8.2E-02 P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR
4187	14087	23864		5.36	8.2E-02 P48960	SWISSPROT	LEUCOCYTE ANTIGEN CD97 PRECURSOR

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5014	14888	246555	2.82	8.2E-02	U76009.1	NT	<i>Mus musculus</i> zinc transporter (Znt-3) gene, complete cds
5271	15193	24988	1.43	8.2E-02	BE897030.1	EST_HUMAN	601439676F1 NIH_MGC_72 <i>Homo sapiens</i> cDNA clone IMAGE:3924523 5'
6188	16073	26222	3.14	8.2E-02	AF5309855.1	NT	<i>Bos taurus</i> connective tissue growth factor precursor (CTGF) gene, complete cds
7094	16971	27164	3.13	8.2E-02	AW875126.1	EST_HUMAN	RC2-PT0004-03/299-011-005 PT0004 <i>Homo sapiens</i> cDNA
7556	17387	27598	5.33	8.2E-02	X04197.1	NT	Beet necrotic yellow vein virus RNA-2
7628	17479	27699	2.11	8.2E-02	BE254318.1	EST_HUMAN	601113055F1 NIH_MGC_16 <i>Homo sapiens</i> cDNA clone IMAGE:3356596 5'
9314	19006	25336	4.13	8.2E-02	AE002246.2	NT	<i>Chlamydophila pneumoniae</i> AR39, section 73 of 94 of the complete genome
9708	19480			1.84	8.2E-02	AF275366.1	<i>Mus musculus</i> epidermal growth factor receptor (Egrfr) gene, exons 5 through 28, and complete cds, alternatively spliced
1479	11384	21247	1.72	8.1E-02	AB017138.1	NT	<i>Pseudomonas putida</i> malonate decarboxylase gene cluster (mdcA, mdcB, mdcC, mdcD, mdcE, mdcG, mdch, mdcl and mdcm genes), complete cds
7703	17553			1.65	8.1E-02	AB005150.1	<i>Homo sapiens</i> chromosome 21 segment HS21C002
8789	18804	28894	3.38	8.1E-02	AL163202.2	NT	<i>Homo sapiens</i> chromosome 21 segment HS21C002
5	12557	19784	3.28	8.0E-02	AW954663.1	EST_HUMAN	EST368723 MAGE resequences, MAGE <i>Homo sapiens</i> cDNA
920	10844	20690	1.33	8.0E-02	U60315.1	NT	<i>Molluscum contagiosum</i> virus subtype 1, complete genome
1671	12701	21440	10.54	8.0E-02	D28535.1	NT	Human gene for dihydroxyacetone succinyltransferase, complete cds (exon 1-15)
1671	12701	21441	10.54	8.0E-02	D28535.1	NT	Human gene for dihydroxyacetone succinyltransferase, complete cds (exon 1-15)
1861	11757	21632	3.9	8.0E-02	BE067219.1	EST_HUMAN	PM3-BT0347-17020-001-008 BT0347 <i>Homo sapiens</i> cDNA
2323	12204	22103	1.01	8.0E-02	D00915.1	NT	<i>Synechocystis</i> sp. PCC6503 complete genome, 17/27, 21/37259-2267259
2323	12204	22104	1.01	8.0E-02	D00915.1	NT	<i>Synechocystis</i> sp. PCC6503 complete genome, 17/27, 21/37259-2267259
2421	12298			4.08	8.0E-02	BE246744.1	EST_HUMAN
2790	10991	20853	0.81	8.0E-02	M23449.1	NT	Dichocyphium discoideum cyclic nucleotide phosphodiesterase gene, complete cds
2870	12797	22591	1.01	8.0E-02	AL445067.1	NT	<i>Thermoplasma acidophilum</i> complete genome, segment 5/5
31745	13558	23440	0.84	8.0E-02	AW966118.1	EST_HUMAN	EST373101 MAGE resequences, MAGE <i>Homo sapiens</i> cDNA
3980	13887			1.06	8.0E-02	4503034 NT	<i>Homo sapiens</i> c-MMP responsive element binding protein-like 2 (GREBL2) mRNA
4709	14595			5.62	8.0E-02	X72794.1	<i>M.musculus</i> gene for gelatinase B
4834	14716	24499	0.87	8.0E-02	M28071.1	NT	<i>Herpesvirus saimiri</i> transformation-associated protein (STP), and dihydrofolate reductase (DHFR) gene, s complete cds, and small nuclear RNAs (uRNAs)
5591	15506	25581	3.35	8.0E-02	AF275948.1	NT	<i>Homo sapiens</i> ABCA1 (ABCA1) gene, complete cds
6261	15506	25581	1.63	8.0E-02	AF275948.1	NT	<i>Homo sapiens</i> ABCA1 (ABCA1) gene, complete cds
6727	16607	26798	3.65	8.0E-02	AL114993.1	NT	<i>Batrachium cinereum</i> strain T4 cDNA library under conditions of nitrogen deprivation
7401	17268	27471	1.49	8.0E-02	X74208.1	NT	<i>H.sapiens</i> AGT gene, intron 4
7401	17268	27472	1.49	8.0E-02	X74208.1	NT	<i>H.sapiens</i> AGT gene, intron 4

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8172	18060	28310	7.42	8.0E-02	AF217796.1	NT	Homo sapiens SCG10 like-protein, helicase-like protein NIH, M68, and ADP-ribosylation factor related protein 1 (ARFRP1) genes, complete cds
9344	19023	26300	2.94	8.0E-02	AJ005375.1	NT	Drosophila orena runt/brach region
9891	13887		1.47	8.0E-02	4503034	NT	Homo sapiens cAMP responsive element binding protein-like 2 (CREBL2) mRNA
9969	19654		3.04	8.0E-02	AJ278425.1	NT	Mus musculus Ranbp7 gene, Stat gene and Wee1 gene
2127	12015	21913	3.98	7.9E-02	BE250008.1	EST_HUMAN	600943191F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959510 5' er98c0x1 Barstead colon HPLRB7 Homo sapiens cDNA clone IMAGE:2173646 3' similar to gb:Z228876
2948	12875	22673	6.43	7.9E-02	AJ582029.1	EST_HUMAN	60S RIBOSOMAL PROTEIN L38 (HUMAN);
3776	13688	23471	3.31	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csfr1), mRNA
3776	13688	23472	3.31	7.9E-02	6681044	NT	Mus musculus colony stimulating factor 1 receptor (Csfr1), mRNA
4595	14483	24269	1.06	7.9E-02	BF348454.1	EST_HUMAN	602019770F1 NCI_CGAP_Bm67 Homo sapiens cDNA clone IMAGE:4155401 5'
4706	14592		1.16	7.9E-02	AB008019.1	NT	Arabidopsis thaliana RXW24L mRNA, partial cds
6682	16562	26756	3.25	7.9E-02	U27832.1	NT	Saccharomyces cerevisiae suppressor of MIF2 Sm14p (SMF4) gene, complete cds
7762	17612	27838	5.68	7.9E-02	A1081644.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WF:CS7A2.2 CE08611;
7762	17612	27839	5.68	7.9E-02	A1081644.1	EST_HUMAN	ou63b05.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632465 3' similar to WF:CS7A2.2 CE08611;
1192	11102	20947	1.43	7.8E-02	A1793275.1	EST_HUMAN	cc59d02.5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L113 L1 repetitive element;
1192	11102	20948	1.43	7.8E-02	A1783275.1	EST_HUMAN	cc59d02.5 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570467 5' similar to contains L113 L1 repetitive element;
4688	14574	24371	0.81	7.8E-02	BE856331.1	EST_HUMAN	PM3-FN0058-140700-005-009 FN0058 Homo sapiens cDNA
5019	13603		2.71	7.8E-02	BE250048.1	EST_HUMAN	600943055F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:2959693 5'
5197	15060	24825	1.04	7.8E-02	A1418520.1	EST_HUMAN	tg48g12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2112070 3' similar to contains MER10.13 MER10 repetitive element;
7236	17113	27306	2.06	7.8E-02	AF2383437.1	NT	Homo sapiens FVVE domain-containing dual specificity protein phosphatase FVVE-DSPIb mRNA, complete cds
7236	17113	27307	2.06	7.8E-02	AF2383437.1	NT	Homo sapiens FVVE domain-containing dual specificity protein phosphatase FVVE-DSPIb mRNA, complete cds
7389	17307	27513	1.27	7.8E-02	AA469354.1	EST_HUMAN	nc68b06.r1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:771731
1378	12693	21139	1	7.7E-02	AF181897.1	NT	Homo sapiens WRN (WRN) gene, complete cds
3538	13454		2.09	7.7E-02	AJ528093.1	NT	Homo sapiens partial AF-4 gene, exons 2 to 7 and All repeat elements
6615	16495	26682	4.4	7.7E-02	AA402949.1	EST_HUMAN	zut53d11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:741717 5' similar to TR:G1173905 G1173905 SPLICEOSOME ASSOCIATED PROTEIN ;

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7660	17510	27736	4.62	7.7E-02	P38080	SWISSPROT	PROBABLE SERINE/THREONINE-PROTEIN KINASE (BR059C
8376	18253	28504	5.24	7.7E-02	11422757	NT	Hom sapiens KIAA0628 gene product (KIAA0628), mRNA
9535	19561		2	7.7E-02	11436559	NT	Hom sapiens Interferon regulatory factor 7 (IRF7), mRNA
3341	13261	23067	2.57	7.6E-02	BE514432.1	EST_HUMAN	601316_426F1 NIH_MIGC_8 Homo sapiens cDNA clone IMAGE:3634903 5'
3362	13281	23081	0.94	7.6E-02	AA296447.1	EST_HUMAN	EST112214 Cerebellum II Homo sapiens cDNA 5' end similar to prococadherin 43
3512	13428	28229	0.93	7.6E-02	AJ400877.1	NT	Hom sapiens ASCL3 gene, CEGF1 gene, C11orf14 gene, C11orf15 gene, C11orf16 gene and C11orf17 gene
4765	14650		0.96	7.6E-02	AWB58844.1	EST_HUMAN	RC3-C70347-11030-014-a05 CT0347 Homo sapiens cDNA
7393	17311	27518	1.34	7.6E-02	AJ131016.1	NT	Hom sapiens SCL gene locus
7695	17545		1.34	7.6E-02	AL139078.2	NT	Campylobacter jejuni NCTC1168 complete genome; segment 5/6
8927	18736	29028	2.45	7.6E-02	AW998645.1	EST_HUMAN	QV3-BN0046-15040-01-51-004 BN0046 Homo sapiens cDNA
767	10698	20535	1.13	7.5E-02	5902093	NT	Hom sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
767	10698	20536	1.13	7.5E-02	5902093	NT	Hom sapiens solute carrier family 6 (neurotransmitter transporter, glycine), member 9 (SLC6A9), mRNA
1878	11774	21649	0.87	7.5E-02	AL163278.2	NT	Hom sapiens chromosome 21 segment HS21C078
4407	14301	24085	0.84	7.5E-02	AB015061.1	NT	Hom sapiens IL-18 gene for interleukin-18, intron 1 and exon 2
6855	16734	26927	1.19	7.5E-02	A1864367.1	EST_HUMAN	wi52b02,x1 NCI CGAP_Bm25 Homo sapiens cDNA clone IMAGE:2428491 3' similar to gb: M14328 ALPHA ENOLASE (HUMAN);
6953	16831	27024	1.21	7.5E-02	AU1116913.1	EST_HUMAN	AU116913 HEMBA1 Homo sapiens cDNA clone HEMBA1000264 5'
469	10412	20231	1.23	7.4E-02	AW838547.1	EST_HUMAN	RC5-LT005-L-260100-011-H09 LT0054 Homo sapiens cDNA
1444	11349		1.08	7.4E-02	AF030227.1	NT	Equine herpesvirus 4 strain NS80567, complete genome
2536	12410		0.93	7.4E-02	6755069	NT	Mus musculus paired-like homeodomain transcription factor 1 (Pbx1), mRNA
3545	13461	23255	0.89	7.4E-02	A1807885.1	EST_HUMAN	wf49h01,x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2558385 3'
4606	14494	24282	3.38	7.4E-02	L75810.1	NT	Hom sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds
4687	14573	24370	2.66	7.4E-02	6978442	NT	Rattus norvegicus Activin receptor like kinase 1 (Acvr1), mRNA
4858	14738	24518	1.7	7.4E-02	6678492	NT	Mus musculus ubiquitin c-terminal hydrolase related polypeptide (Uchp), mRNA
5913	15819		1.75	7.4E-02	R17477.1	EST_HUMAN	Ygt4g06_r1 Soares infant brain NIB_Homo sapiens cDNA clone IMAGE:32339 5'
6612	16492	28678	1.4	7.4E-02	BE880112.1	EST_HUMAN	601493366F1 NIH_MIGC_69 Homo sapiens cDNA clone IMAGE:3895264 5'
6950	16828	27021	1.37	7.4E-02	U56089.1	NT	Human periodic tryptophan protein 2 (PWP2) gene, exons 15 to 21, and complete cds
9271	18975		2.08	7.4E-02	11425893	NT	Hom sapiens histone deacetylase 5 (NY-CO-9), mRNA
9527	19674		2.82	7.4E-02	AW379431.1	EST_HUMAN	CMA-HT0243-081198-037-d11 HT0243 Homo sapiens cDNA
9678	19235	25242	1.81	7.4E-02	BF035098.1	EST_HUMAN	601453-813F1 NIH_MIGC_66 Homo sapiens cDNA clone IMAGE:3857738 5'
461	10405	20222	0.96	7.3E-02	BE964961.2	EST_HUMAN	601688738R1 NIH_MIGC_69 Homo sapiens cDNA clone IMAGE:3886209 3'

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Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
461	10405	20223	0.96	7.3E-02	BE964961.2	EST_HUMAN	6016658738821 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:33886209 3'
669	10603	20420	2.73	7.3E-02	AE001789.1	NT	Thermotoga maritima section 101 of 136 of the complete genome
1465	12695	21237	3.04	7.3E-02	AW1900281.1	EST_HUMAN	CM0-NN1004-130300-284-g08 NN1004 Homo sapiens cDNA
1801	12705		14.81	7.3E-02	AL168302.2	NT	Homo sapiens chromosome 21 segment HS21C102
4927	14806		1.01	7.3E-02	U12283.1	NT	Mus musculus transcription factor USF2 (USF2) gene, exons 8-10 and complete cds
6413	16275	26437	2.44	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
6413	16275	26138	2.44	7.3E-02	P05143	SWISSPROT	PROLINE-RICH PROTEIN MP-3
6749	16628		1.27	7.3E-02	7662107	NT	Homo sapiens KIAA0424 protein (KIAA0424), mRNA
8548	15788	25910	2.78	7.3E-02	AA779977.1	EST_HUMAN	224a02.s1 Soares_fetal_liver_spleen_1NF1S_S1 Homo sapiens cDNA clone IMAGE:451178 3' similar to gb:LC0426 26S PROTEASE SUBUNIT 4 (HUMAN);
114	10093	19911	0.94	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
114	10093	19912	0.94	7.2E-02	AE000882.1	NT	Methanobacterium thermoautotrophicum from bases 1029155 to 1039934 (section 88 of 148) of the complete genome
1460	11365	21228	2.23	7.2E-02	AL168301.2	NT	Homo sapiens chromosome 21 segment HS21C101
1460	11365	21229	2.23	7.2E-02	AL168301.2	NT	Homo sapiens chromosome 21 segment HS21C101
2502	12377		2.5	7.2E-02	U14794.1	NT	Human immunodeficiency virus type 1 isolate 26 reverse transcriptase (pol) gene, internal fragment, partial cds
3810	13722	23511	0.82	7.2E-02	AW1298322.1	EST_HUMAN	U1-H-BW0-all-a-0-0-U1_s1 NCI_CGAP_SubS Homo sapiens cDNA clone IMAGE:2732049 3'
4249	14148	23922	4.02	7.2E-02	BF572307.1	EST_HUMAN	60207757F1 NIH_MGC_62 Homo sapiens cDNA clone IMAGE:4251950 5'
4594	14482	24268	78.82	7.2E-02	11466383	NT	Rhodomonas salina mitochondrion, complete genome
4997	14872	24636	0.94	7.2E-02	AB001562.1	NT	Streptococcus mutans gene for glucose-1-phosphate uridylyltransferase, complete cds
5230	15154	24922	3.03	7.2E-02	U67531.1	NT	Methanococcus jannaschii section 73 of 150 of the complete genome
5231	15155	24923	7.62	7.2E-02	P11120	SWISSPROT	CALMODULIN
6252	16118	26272	9.33	7.2E-02	BF216086.1	EST_HUMAN	6016835556F1 NIH_MGC_57 Homo sapiens cDNA clone IMAGE:4095710 5'
6281	16145		1.75	7.2E-02	5834897	NT	Strongylocentrotus purpuratus mitochondrion, complete genome
7545	17396	27608	2.05	7.2E-02	AV712452.1	EST_HUMAN	AV712452 DCA Homo sapiens cDNA clone DCAAUG01 5'
7625	17476	27697	4.23	7.2E-02	L14561.1	NT	Homo sapiens plasma membrane calcium ATPase isoform 1 (ATP2B1) gene, alternative splice products, partial cds
7746	17596	27818	2.64	7.2E-02	AW1873187.1	EST_HUMAN	hq24f11.x1 NCI_CGAP_Ad1 Homo sapiens cDNA clone IMAGE:3120333 3' similar to TR:Q9Z340 Q9Z340 ATYPICAL PKC SPECIFIC BINDING PROTEIN.;
7926	17776	28016	2.05	7.2E-02	U82695.2	NT	Homo sapiens zinc finger protein 92 (ZFP92), expressed-Xq28STS protein (XQ28ORF), and biglycan (BGN) genes, complete cds; and plasma membrane calcium ATPase isoform 3 (PMCA3) gene, partial cds

Table 4
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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
7983	17833	28073	5.47	7.2E-02	BE565003.1	EST_HUMAN	601343926F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3685956 5'
7984	17844		3.2	7.2E-02	BE539214.1	EST_HUMAN	601065194F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3451559 5'
8285	18164	28407	4.8	7.2E-02	AF049874.1	NT	Rattus norvegicus bHLH transcription factor Mist1 (Mist1) gene, complete cds
9178	18919	25346	1.44	7.2E-02	AA73896.1	EST_HUMAN	af81a04.11 Soares_NIHMPu_S1 Homo sapiens cDNA clone IMAGE:1048398 5'
9214	18942		3.13	7.2E-02	AJ230796.1	EST_HUMAN	AJ230796 Homo sapiens library (Seranski P) Homo sapiens cDNA clone PS13D5 3'
9273	18977		1.44	7.2E-02	AA584465.1	EST_HUMAN	nc00508.s1 NCI_CGAP_Pne1 Homo sapiens cDNA clone IMAGE:1089839 3'
9332	19013		1.62	7.2E-02	U82828.1	NT	Homo sapiens ataxia telangiectasia (ATM) gene, complete cds
9346	19531		3.89	7.2E-02	AW300962.1	EST_HUMAN	CM4-NN1009-203004-116-c11 NN1009 Homo sapiens cDNA
1882	11758	21633	1.65	7.1E-02	U02290.1	NT	Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds
2243	12127		0.9	7.1E-02	AE04890.1	NT	Pseudomonas aeruginosa PA01, section 451 of 529 of the complete genome
2247	12131	22028	5.08	7.1E-02	BF208802.1	EST_HUMAN	601872281F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4082981 5'
9063	18844		4.98	7.1E-02	BE304764.1	EST_HUMAN	601143974F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:3061234 5'
517	10459	20270	1.23	7.0E-02	Q07092	SWISSPROT	COLLAGEN ALPHA 1(XV) CHAIN PRECURSOR
1484	11389		1.46	7.0E-02	X96677.1	NT	Martellia Micut-1 gene
1725	11626	21495	1.36	7.0E-02	AA056343.1	EST_HUMAN	Zf6874.s1 Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:5095639 3'
2994	12922	22715	1.72	7.0E-02	AW138152.1	EST_HUMAN	Ui-H-B11-acy-c-07-0-I1.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone IMAGE:2716020 3'
					ai65a12.s1 Soares,testis_NHT Homo sapiens cDNA clone 1375678 3' similar to gb:K03002 605		
3822	13734	23523	1	7.0E-02	AA815438.1	EST_HUMAN	RIBOSOMAL PROTEIN L32 (HUMAN);
3958	13866	23642	1.24	7.0E-02	BE070264.1	EST_HUMAN	QV4-BT0407-280100-000-e10 BT0407 Homo sapiens cDNA
4047	13949		1.08	7.0E-02	AW702962.1	EST_HUMAN	CM0-U0001-060300-270-e12 UM0001 Homo sapiens cDNA
4121	14021	23709	1.27	7.0E-02	AF077821.1	NT	Canis familiaris inducible nitric oxide synthase mRNA, complete cds
4846	14727	24510	7.1	7.0E-02	BF381987.1	EST_HUMAN	601816291F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4050071 5'
7259	17436	27329	1.25	7.0E-02	9628113	NT	African swine fever virus, complete genome
7334	17385	27597	1.19	7.0E-02	K02901.1	NT	Rat Ig germline epsilon H-chain gene C-region, 3' end
					ah92a05.s1 SoaresNFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1327184 3' similar to gb:L14837		
8679	18567	28830	2.39	7.0E-02	AA724295.1	EST_HUMAN	TIGHT JUNCTION PROTEIN ZO-1 (HUMAN);
503	10445	20286	5.34	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
503	10445	20287	5.34	6.9E-02	AL163210.2	NT	Homo sapiens chromosome 21 segment HS21C010
1311	11217		1.31	6.9E-02	4507968	NT	Homo sapiens regulator of Gz-selective protein signalling (ZGAP1) mRNA, and translated products
3724	13636	23421	1.42	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D)
3724	13636	23422	1.42	6.9E-02	Q06364	SWISSPROT	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D)
5100	14868		1.05	6.9E-02	AF079806.1	NT	Rabies virus isolate b615 glycoprotein gene, partial cds

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
6978	16855	27048	1.37	6.9E-02	BE567435.1	EST_HUMAN	601340661 F1 NIH_MGCC_53 Homo sapiens cDNA clone IMAGE:36883030 5'
6978	16855	27049	1.37	6.9E-02	BE567435.1	EST_HUMAN	601340661 F1 NIH_MGCC_53 Homo sapiens cDNA clone IMAGE:36883030 5'
9208	18939		3.95	6.9E-02	X74315.1	NT	X.laevis XFD2 mRNA for fork head protein
9355	19045		1.5	6.9E-02	P44621	SWISSPROT	PROTEIN TRANSPORT PROTEIN HOFC HOMOLOG
9558	19180		2.19	6.9E-02	AF1985953.1	NT	Homo sapiens membrane-bound aminopeptidase P (XNPEP2) gene, complete cds
1839	11736	21610	1.11	6.8E-02	AA495759.1	EST_HUMAN	aa30102.1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1839	11736	21611	1.11	6.8E-02	AA495759.1	EST_HUMAN	aa30102.1 Gessler Wilms tumor Homo sapiens cDNA clone IMAGE:897339 5' similar to gb:M22382
1865	11761	21635	3.91	6.8E-02	AF156673.1	NT	Homo sapiens putative hepatic transcription factor (WBSCTR14) gene, complete cds
3062	12989	22780	1.23	6.8E-02	AA781996.1	EST_HUMAN	ai75a06.s1 Soares testis_NHT Homo sapiens cDNA clone 1376626 3'
3062	12989	22781	1.23	6.8E-02	AA781996.1	EST_HUMAN	ai75a06.s1 Soares testis_NHT Homo sapiens cDNA clone 1376626 3'
3062	12989	22782	1.23	6.8E-02	AA781996.1	EST_HUMAN	ai75a06.s1 Soares testis_NHT Homo sapiens cDNA clone 1376626 3'
4453	14347		0.92	6.8E-02	BE141076.1	EST_HUMAN	MR0-HT0069-071099-001-c05 HT0069 Homo sapiens cDNA
6315	16178	26337	7.71	6.8E-02	AL163268.2	NT	Homo sapiens chromosome 21 segment HS21C068
6622	16701	26894	6.12	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 5/6
6822	16701	26895	6.12	6.8E-02	AJ248287.1	NT	Pyrococcus abyssi complete genome, segment 5/6
9011	19719		1.37	6.8E-02	T03214.1	EST_HUMAN	FBA48 3' end similar to LINE-1
9140	18895		2.98	6.8E-02	AA758014.1	EST_HUMAN	aa6705.s1 Soares testis_NHT Homo sapiens cDNA clone 1320705 3'
9164	19284		2.97	6.8E-02	9910535.1	NT	Mus musculus latent TGF beta binding protein (Tgfb), mRNA
1511	11416		2.17	6.7E-02	AF115536.1	NT	Oncorhynchus mykiss TAP1 protein (OmyTAP1) mRNA, OnmyTAP1 allele, complete cds
1881	11747	21622	2.5	6.7E-02	AI220285.1	EST_HUMAN	gg79e04.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1841406 3'
3666	13570	23356	3.52	6.7E-02	P17278	SWISSPROT	HOMEobox PROTEIN HOXD4 (CHTOX-A)
1326	11233	21089	1.05	6.6E-02	AI735509.1	EST_HUMAN	ai12e09.x1 Barstetta anta HPLRB6 Homo sapiens cDNA clone IMAGE:2354920 3' similar to SW:LIN1_NYCCO P08548 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. ;
1347	11253	21109	1.5	6.6E-02	AF245116.1	NT	Drosophila melanogaster cactin mRNA, complete cds
2133	12021	21918	3.07	6.6E-02	AJ289244.1	NT	Mus musculus Capn12 gene for calbindin 12, exons 1-21, three alternative transcripts
3133	13058		1.32	6.6E-02	Q13585	SWISSPROT	MELATONIN-RELATED RECEPTOR (H9)
3418	13335	23139	8.61	6.6E-02	R64306.1	EST_HUMAN	yi18b10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139578 3'
3492	13349	23154	2.19	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3492	13349	23155	2.19	6.6E-02	7108357	NT	Homo sapiens mesothelin (MSLN), transcript variant 1, mRNA
3889	13396	23673	1.59	6.6E-02	AF260225.1	NT	Homo sapiens TESTIN 2 and TESTIN 3 genes, complete cds, alternatively spliced
4904	14784	24558	8.4	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)
4904	14784	24559	8.4	6.6E-02	Q61703	SWISSPROT	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR (ITI HEAVY CHAIN H2)

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
5167	15033	24800		1.34	6.6E-02 AF204882.1	NT	<i>Amesacta albiflriga nucleopolyhedrovirus AcORF17 homolog gene, complete cds</i>
5190	15053	24817		0.84	6.6E-02 AE049345.1	NT	<i>Vibrio cholerae chromosome II, section 2 of 93 of the complete chromosome</i>
5968	15873	25998		3.09	6.6E-02 X06411.1	NT	<i>P.vulgaris mRNA for chalcone synthase</i>
6209	15969	26105		2.93	6.6E-02 AI24326.1	EST_HUMAN	<i>qtl41d01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:1847233 3'</i>
6635	16515	26706		1.48	6.6E-02 AF052572.1	NT	<i>Homo sapiens chemokine receptor CXCR4 gene, promoter region and complete cds</i>
7806	17656	27894		1.37	6.6E-02 Y07348.1	NT	<i>Homo sapiens EW5, qtl22, np22 and bam22 genes</i>
8330	18207	28457		6.28	6.6E-02 BF374248.1	EST_HUMAN	<i>MR1-SN0064-010500-006-af2 SN0064 Homo sapiens cDNA</i>
9593	19175			2.08	6.6E-02 9937991	NT	<i>Mus musculus DIPB gene (Dipb), mRNA</i>
9882	19366			1.46	6.6E-02 AF167430.1	NT	<i>Rattus norvegicus cytochrome P450 2E1 (CYP2E1) gene, 5' flanking region</i>
567	10506	20313		1.91	6.5E-02 BF027639.1	EST_HUMAN	<i>601671046F1 NIH MGC_20 Homo sapiens cDNA clone IMAGE:3954478 5'</i>
971	10895	20743		1.75	6.5E-02 7706098	NT	<i>Homo sapiens E2F-like protein (LOC51270), mRNA</i>
1369	11275	21131		4.17	6.5E-02 U47624.1	NT	<i>Xenopus laevis alpha(E)-catenin mRNA, complete cds</i>
1702	11603	21474		2.16	6.5E-02 AE000764.1	NT	<i>Aquifex aeolicus section 96 of 109 of the complete genome</i>
5413	15333	25383		1.76	6.5E-02 AA443991.1	EST_HUMAN	<i>zv46n12.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:756743 3' similar to gb:M26038 HLA CLASS II HISTOCOMPATIBILITY ANTIGEN DR-5 BETA CHAIN (HUMAN);</i>
8035	17927	28173		5.61	6.5E-02 AA195648.1	EST_HUMAN	<i>zr32g05.s1 Soares_NHMP4_S1 Homo sapiens cDNA clone IMAGE:865144 3'</i>
9034	18823			3.53	6.5E-02 M21496.1	NT	<i>Rabbit microsomal epoxide hydrolase</i>
9393	19051			3.73	6.5E-02 AF12993.1	NT	<i>Nectria haematococca kinesin related protein 2 (KRP2) gene, complete cds</i>
561	10501	20307		1.53	6.4E-02 X94549.1	NT	<i>A carboxy precursor of peridinin-chlorophyll a protein (PCP) gene</i>
4802	12909	22708		1.35	6.4E-02 6996923	NT	<i>Mus musculus histone deacetylase 5 (Hdac5), mRNA</i>
5180	15044			8.78	6.4E-02 6996923	NT	<i>Mus musculus histone deacetylase 5 (Hdac5), mRNA</i>
5346	15267	25094		1.4	6.4E-02 AI191956.1	EST_HUMAN	<i>q070501.x1 Soares_NHT Homo sapiens cDNA clone IMAGE:1738249 3' similar to contains LTR8.b3 LTR8 repetitive element;</i>
5748	15625	25727		7.58	6.4E-02 AF052733.1	NT	<i>Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-gn-1) gene, complete cds</i>
5718	15625	25728		7.58	6.4E-02 AF052733.1	NT	<i>Heterodera glycines beta-1,4-endoglucanase-1 precursor (HG-gn-1) gene, complete cds</i>
6079	16062	26210		5.23	6.4E-02 BE974448.1	EST_HUMAN	<i>601680425R2 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:3950503 3'</i>
6883	16732			2.57	6.4E-02 6753323	NT	<i>Mus musculus chaperonin subunit 6a (zeta) (Cct6a), mRNA</i>
7034	16911	27059		4.12	6.4E-02 AA093305.1	EST_HUMAN	<i>kr1419.sseq.F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'</i>
7603	17454	27668		2.02	6.4E-02 AB011126.1	NT	<i>Homo sapiens mRNA for KIAA0554 protein, partial cds</i>
8946	18754	29049		1.86	6.4E-02 U91328.1	NT	<i>Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RnRt gene, and sodium phosphate transporter (NPT3) gene, complete cds</i>

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Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
8946	18754	29050		1.86	6.4E-02 U91328.1	NT	Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, RoRef gene, and sodium phosphate transporter (NPT3) gene, complete cds
9289	19635	—		3.65	6.4E-02 AF0107890.1	NT	Homo sapiens mucin 5B (MUC5B) gene, partial cds
9337	19017	25295		2.27	6.4E-02 AJ277174.1	NT	Drosophila melanogaster mRNA for mod(mdg4)51.4 protein
1720	11621	21490		2.43	6.3E-02 AF109905.1	NT	
3552	13467	—		2.09	6.3E-02 P37092	SWISSPROT	HEAT SHOCK PROTEIN 70 HOMOLOG
7752	17602	27825		3.14	6.3E-02 AB010162.1	NT	Hepatitis G virus RNA for polyprotein (NS5A region), partial cds, strain: CMR-152
8098	15637	25741		3.29	6.3E-02 BF210736.1	EST_HUMAN	601873316F1 NIH-MGC_54 Homo sapiens cDNA clone MAGE-4097498 5'
9373	19039	—		1.49	6.3E-02 P15276	SWISSPROT	TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALG3)
4157	14057	23831		3.37	6.2E-02 AL161572.2	NT	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 68
4243	14142	—		1.11	6.2E-02 AF271235.1	NT	Rattus norvegicus differentiation-associated Na-dependent inorganic phosphate cotransporter (DNPi) mRNA, complete cds
4479	14373	—		5.41	6.2E-02 Q62191	SWISSPROT	52 KIDRO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SSA)) (RO52)
4803	14687	—		1.22	6.2E-02 AV705701.1	EST_HUMAN	AV705701 ADB Homo sapiens cDNA clone ADBBAB03 5'
7459	17319	27525		1.21	6.2E-02 6977588	NT	Mus musculus stromal cell derived factor receptor 2 (Sdf2), mRNA
8655	18544	28827		1.84	6.2E-02 AJ242735.1	NT	Metarhizium anisopliae mRNA for Chymotrypsin (chv1 gene)
9129	19752	—		3.53	6.2E-02 AE000750.1	NT	Aquifex aeolicus section 82 of 109 of the complete genome
9541	19142	25265		1.98	6.2E-02 BF112039.1	EST_HUMAN	7137h08_x1 Soares_NSF_F8_9W_OT_PA_P_S Homo sapiens cDNA clone IMAGE:3523815 3' similar to TR:Q9J4S6 Q9Y4S6 HYPOTHETICAL 30.3 KD PROTEIN. [1];
256	10222	20038		4.53	6.1E-02 D16471.1	NT	Human mRNA, Xq terminal portion
3909	13819	—		2.65	6.1E-02 U73325.1	NT	Arabidopsis thaliana K+-inward rectifying channel protein (AtKC1) gene, complete cds
5150	15017	24785		1.01	6.1E-02 AB040897.1	NT	Homo sapiens mRNA for KIAA1464 protein, partial cds
6809	16688	28877		3.46	6.1E-02 X99268.1	NT	H. sapiens mRNA for B-H-LH DNA binding protein
8112	18002	28248		5.44	6.1E-02 BE179543.1	EST_HUMAN	IL3-HT0618-110500-138-C06 HT0618 Homo sapiens cDNA
9088	19670	—		7.17	6.1E-02 X70989.1	NT	S. japonicum mRNA for serine-enzyme
9783	19296	—		3.6	6.1E-02 AL163207.2	NT	Homo sapiens chromosome 21 segment HS21C007
1241	11148	20997		1.41	6.0E-02 AE001777.1	NT	Thermotoga maritima section 89 of 136 of the complete genome
2641	12508	22399		1.57	6.0E-02 AW968848.1	EST_HUMAN	EST38924 MAGE resequences, MAGU1 Homo sapiens cDNA
2745	12607	—		1.61	6.0E-02 AB031289.1	NT	Mesocystoides cont mithochondrial DNA, NADH dehydrogenase subunit 4, tRNA-Gln, tRNA-Phe, tRNA-Met, ATPase subunit 6, and NADH dehydrogenase subunit 2
2806	10076	19892		1.22	6.0E-02 AA188730.1	EST_HUMAN	2p78c04.11 Stratagene HeLa cell ss 937216 Homo sapiens cDNA clone IMAGE:628310 5'

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 Single Exon Probes Expressed in Heart

Probe SEQ ID NO:	Exon SEQ ID NO:	ORF SEQ ID NO:	Expression Signal	Most Similar (Top) Hit BLAST E Value	Top Hit Accession No.	Top Hit Database Source	Top Hit Descriptor
2906	10076	19893		1.22	6.0E-02 AA1887930.1	EST_HUMAN	zp78c04,r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:6226310 5'
3191	13116	22921		1.2	6.0E-02 AA372376.1	EST_HUMAN	EST84266 Colon adenocarcinoma, IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3191	13116	22922		1.2	6.0E-02 AA372376.1	EST_HUMAN	EST84266 Colon adenocarcinoma, IV Homo sapiens cDNA 5' end similar to tissue-specific protein
3583	13497			0.9	6.0E-02 BE94443.2	EST_HUMAN	601658150R1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3876060 3'
4893	14773	24551		1.17	6.0E-02 Z57739.2	NT	Streptococcus pneumoniae patC, patE and transposase genes and ORF DNA
5314	15235			3.46	6.0E-02 AW370211.1	EST_HUMAN	RC3-BT0253-01/1199-013-b04 BT0253 Homo sapiens cDNA
6172	15129	24848		2.86	6.0E-02	5174698 NT	Homo sapiens stimulated trans-acting factor (50 kDa) STAF50 mRNA
6172	15129	24849		2.86	6.0E-02	5174698 NT	Homo sapiens stimulated trans-acting factor (50 kDa) STAF50 mRNA
6265	16130	26284		1.97	6.0E-02 BF382349.1	EST_HUMAN	601815274F2 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4049226 5'
6524	16383	26562		2.05	6.0E-02 A1204275.1	EST_HUMAN	q58b08_x1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:1754199 3'
7340	17208	27406		1.19	6.0E-02 A1623167.1	EST_HUMAN	ts78ad06_x1 NCI CGAP GCG Homo sapiens cDNA clone IMAGE:2237362 3'
7340	17208	27407		1.19	6.0E-02 A1623167.1	EST_HUMAN	ts78ad06_x1 NCI CGAP GCG Homo sapiens cDNA clone IMAGE:2237362 3'
7411	17228	27486		1.79	6.0E-02 A1245365.1	NT	Acipenser baeri partial GLV gene for Immunoglobulin light chain variable region, exons 1-2
7411	17228	27487		1.79	6.0E-02 A1245365.1	NT	Acipenser baeri partial GLV gene for Immunoglobulin light chain variable region, exons 1-2
9336	19016	25294		1.95	6.0E-02	11431702 NT	Homo sapiens DNA-dependent protein kinase catalytic subunit-interacting protein 2 (KIP2), mRNA
9715	19256			1.84	6.0E-02 A1809273.1	EST_HUMAN	wf8sh03_x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2360885 3' similar to TR:O60298
229	10198	20011		3.42	5.9E-02 AW934719.1	EST_HUMAN	RC1-DT001001-280100-012-e10 DT00101 Homo sapiens cDNA
2955	12882	22681		2.59	5.9E-02 AF+90269.1	NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
4770	14655	24443		0.88	5.9E-02 AF006304.1	NT	Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds
7008	16885	21077		1.87	5.9E-02	9055249 NT	Mus musculus p53 tumor suppressor gene, exon 10 and 11, partial cds; alternatively spliced
8165	18053			2.72	5.9E-02	6679870 NT	Mus musculus iroquois-related homeobox 5 (Drosophila) (lrx5), mRNA
8383	18260	28509		3.15	5.9E-02	11433356 NT	Homo sapiens nhrn (LOC51199), mRNA
8842	18655			1.99	5.9E-02 A1240733.1	NT	Callus gallus HKC9 telomere junction
9117	10841			4.35	5.8E-02 D9010.1	NT	Thiobacillus ferrooxidans merC, merA genes and URF-1
2830	12759			1.1	5.8E-02 AJ223621.1	NT	Populus trichocarpa CCoAOMT1 gene, exon 1 to exon 5
3613	13527	23314		1.44	5.8E-02 AE001775.1	NT	Thermotoga maritima section 87 of 136 of the complete genome
4257	14156	23931		4.36	5.8E-02 AW051927.1	EST_HUMAN	wx24602_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4257	14156	23932		4.36	5.8E-02 AW051927.1	EST_HUMAN	wx24602_x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2544578 3'
4447	14341	24132		4.21	5.8E-02 A1247505.1	EST_HUMAN	qh56f01_x1 Soares fetal liver spleen_1NFSL_S1 Homo sapiens cDNA clone IMAGE:1848897 3' similar to gb:M13192 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4447	14341	24133		4.21	5.8E-02 A1247505.1	EST_HUMAN	qh56f01_x1 Soares fetal liver spleen_1NFSL_S1 Homo sapiens cDNA clone IMAGE:1848897 3' similar to gb:M13192 COAGULATION FACTOR XI PRECURSOR (HUMAN);
4471	14365			2.04	5.8E-02 AF006264.1	NT	Callus gallus tyrosine kinase JAK1 (JAK1) mRNA, complete cds